

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Maertens, Geert
Bosman, Fons
De Martynoff, Guy
Buyse, Marie-Ange

(ii) TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and therapeutic use.

(iii) NUMBER OF SEQUENCES: 122

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: NIXON & VANDERHYE
(B) STREET: 1100 North Glebe Road, 8th Floor
(C) CITY: Arlington, VA 22201
(E) COUNTRY: USA
(F) ZIP: 22201

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DCS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: Unassigned
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Sadoff, B. J.
(B) REGISTRATION NUMBER: 36663
(C) REFERENCE/DOCKET NUMBER: 2551-61

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (703) 816-4000
(B) TELEFAX: (703) 816-4100

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

*All
Cancelled*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCATGCAAG CTTAATTAAT T

21

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CCGGGGAGGC CTGCACGTGA TCGAGGGCAG ACACCATCAC CACCATCACT AATAGTTAAT
TAACTGCA

60

68

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 642 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..639

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTA CTG TCC TGT
Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys
1 5 10 15

48

CTG ACC ATT CCA GCT TCC GCT TAT GAG GTG CGC AAC GTG TCC GGG ATG
Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Met
20 25 30

96

TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG TAT GAG GCA
Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala

144

| 35 | 40 | 45 | |
|---|----|----|-----|
| GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu 50 55 60 | | | 192 |
| AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG CTC GCA GCT Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala 65 70 75 80 | | | 240 |
| AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC GTC GAT TTG Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu 85 90 95 | | | 288 |
| CTC GTT GGG GCG GCT GCT CTC TGT TCC GCT ATG TAC GTG GGG GAT CTC Leu Val Gly Ala Ala Ala Leu Cys Ser Ala Met Tyr Val Gly Asp Leu 100 105 110 | | | 336 |
| TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC TCG CCT CGC Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile Ser Pro Arg 115 120 125 | | | 384 |
| CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His 130 135 140 | | | 432 |
| ATA ACA GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro 145 150 155 160 | | | 480 |
| ACA ACG GCC CTG GTG GTA TCG CAG CTG CTC CGG ATC CCA CAA GCT GTC Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val 165 170 175 | | | 528 |
| GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG GGC CTC GCC Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala 180 185 190 | | | 576 |
| TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT GTG ATG CTA Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu 195 200 205 | | | 624 |
| CTC TTT GCT CTC TAATAG Leu Phe Ala Leu 210 | | | 642 |

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu | Leu | Ser | Cys |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Thr | Ile | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val | Ser | Gly | Met |

| 20 | | | | | | | | | | 25 | | | | | | | | | | 30 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|
| Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val | Tyr | Glu | Ala | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ala | Asp | Met | Ile | Met | His | Thr | Pro | Gly | Cys | Val | Pro | Cys | Val | Arg | Glu | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | 50 | | | | 55 | | | | | 60 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Asn | Asn | Ser | Ser | Arg | Cys | Trp | Val | Ala | Leu | Thr | Pro | Thr | Leu | Ala | Ala | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | 65 | | | 70 | | | | | 75 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Arg | Asn | Ala | Ser | Val | Pro | Thr | Thr | Thr | Ile | Arg | Arg | His | Val | Asp | Leu | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Leu | Val | Gly | Ala | Ala | Ala | Leu | Cys | Ser | Ala | Met | Tyr | Val | Gly | Asp | Leu | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Cys | Gly | Ser | Val | Phe | Leu | Val | Ser | Gln | Leu | Phe | Thr | Ile | Ser | Pro | Arg | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Arg | His | Glu | Thr | Val | Gln | Asp | Cys | Asn | Cys | Ser | Ile | Tyr | Pro | Gly | His | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | 135 | | | | | 140 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ile | Thr | Gly | His | Arg | Met | Ala | Trp | Asp | Met | Met | Met | Asn | Trp | Ser | Pro | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | 145 | | | 150 | | | | 155 | | | | | 160 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Thr | Thr | Ala | Leu | Val | Val | Ser | Gln | Leu | Leu | Arg | Ile | Pro | Gln | Ala | Val | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | 165 | | | | 170 | | | | | 175 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Val | Asp | Met | Val | Ala | Gly | Ala | His | Trp | Gly | Val | Leu | Ala | Gly | Leu | Ala | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | 180 | | | | 185 | | | | | 190 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Tyr | Tyr | Ser | Met | Val | Gly | Asn | Trp | Ala | Lys | Val | Leu | Ile | Val | Met | Leu | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | 195 | | | | 200 | | | | | | 205 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Leu | Phe | Ala | Leu | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | 210 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 795 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..792

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | TTG | GGT | AAG | GTC | ATC | GAT | ACC | CTT | ACA | TGC | GGC | TTC | GCC | GAC | CTC | 48 |
| Met | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| GTG | GGG | TAC | ATT | CCG | CTC | GTC | GGC | GCC | CCC | CTA | GGG | GGC | GCT | GCC | AGG | 96 |
| Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu | Gly | Gly | Ala | Ala | Arg | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| GCC | CTG | GCG | CAT | GGC | GTC | CGG | GTT | CTG | GAG | GAC | GGC | GTG | AAC | TAT | GCA | 144 |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| ACA | GGG | AAT | TTG | CCC | GGT | TGC | TCT | TTC | TCT | ATC | TTC | CTC | TTG | GCT | TTG | 192 |
| Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu | |
| | 50 | | | | 55 | | | | | 60 | | | | | | |
| CTG | TCC | TGT | CTG | ACC | GTT | CCA | GCT | TCC | GCT | TAT | GAA | GTG | CGC | AAC | GTG | 240 |
| Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val | |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | | |
| TCC | GGG | ATG | TAC | CAT | GTC | ACG | AAC | GAC | TGC | TCC | AAC | TCA | AGC | ATT | GTG | 288 |
| Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| TAT | GAG | GCA | GCG | GAC | ATG | ATC | ATG | CAC | ACC | CCC | GGG | TGC | GTG | CCC | TGC | 336 |
| Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr | Pro | Gly | Cys | Val | Pro | Cys | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| GTT | CGG | GAG | AAC | AAC | TCT | TCC | CGC | TGC | TGG | GTA | GCG | CTC | ACC | CCC | ACG | 384 |
| Val | Arg | Glu | Asn | Asn | Ser | Ser | Arg | Cys | Trp | Val | Ala | Leu | Thr | Pro | Thr | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| CTC | GCA | GCT | AGG | AAC | GCC | AGC | GTC | CCC | ACC | ACG | ACA | ATA | CGA | CGC | CAC | 432 |
| Leu | Ala | Ala | Arg | Asn | Ala | Ser | Val | Pro | Thr | Thr | Thr | Ile | Arg | Arg | His | |
| | 130 | | | | | | 135 | | | | | 140 | | | | |
| GTC | GAT | TTG | CTC | GTT | GGG | GCG | GCT | GCT | TTC | TGT | TCC | GCT | ATG | TAC | GTG | 480 |
| Val | Asp | Leu | Leu | Val | Gly | Ala | Ala | Ala | Phe | Cys | Ser | Ala | Met | Tyr | Val | |
| 145 | | | | | 150 | | | | | 155 | | | | 160 | | |
| GGG | GAC | CTC | TGC | GGA | TCT | GTC | TTC | CTC | GTC | TCC | CAG | CTG | TTC | ACC | ATC | 528 |
| Gly | Asp | Leu | Cys | Gly | Ser | Val | Phe | Leu | Val | Ser | Gln | Leu | Phe | Thr | Ile | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| TCG | CCT | CGC | CGG | CAT | GAG | ACG | GTG | CAG | GAC | TGC | AAT | TGC | TCA | ATC | TAT | 576 |
| Ser | Pro | Arg | Arg | His | Glu | Thr | Val | Gln | Asp | Cys | Asn | Cys | Ser | Ile | Tyr | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| CCC | GGC | CAC | ATA | ACG | GGT | CAC | CGT | ATG | GCT | TGG | GAT | ATG | ATG | ATG | AAC | 624 |
| Pro | Gly | His | Ile | Thr | Gly | His | Arg | Met | Ala | Trp | Asp | Met | Met | Met | Asn | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| TGG | TCG | CCT | ACA | ACG | GCC | CTG | GTG | GTA | TCG | CAG | CTG | CTC | CGG | ATC | CCA | 672 |
| Trp | Ser | Pro | Thr | Thr | Ala | Leu | Val | Val | Ser | Gln | Leu | Leu | Arg | Ile | Pro | |
| | | 210 | | | | | 215 | | | | | 220 | | | | |
| CAA | GCT | GTC | GTG | GAC | ATG | GTG | GCG | GGG | GCC | CAT | TGG | GGA | GTC | CTG | GCG | 720 |
| Gln | Ala | Val | Val | Asp | Met | Val | Ala | Gly | Ala | His | Trp | Gly | Val | Leu | Ala | |
| 225 | | | | | 230 | | | | | 235 | | | | 240 | | |
| GGT | CTC | GCC | TAC | TAT | TCC | ATG | GTG | GGG | AAC | TGG | GCT | AAG | GTT | TTG | ATT | 768 |

795

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 263 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

| | | | | | | | | | | | | | | | |
|------------|-----------|------------|------------|-----------|------------|-----------|-----|------------|-----------|------------|------------|------------|------------|------------|------------|
| Met 1 | Leu | Gly | Lys | Val 5 | Ile | Asp | Thr | Leu | Thr 10 | Cys | Gly | Phe | Ala | Asp | Leu 15 |
| Val | Gly | Tyr | Ile 20 | Pro | Leu | Val | Gly | Ala 25 | Pro | Leu | Gly | Gly | Ala 30 | Ala | Arg |
| Ala | Leu | Ala | His 35 | Gly | Val | Arg | Val | Leu 40 | Glu | Asp | Gly | Val 45 | Asn | Tyr | Ala |
| Thr | Gly 50 | Asn | Leu | Pro | Gly | Cys 55 | Ser | Phe | Ser | Ile | Phe 60 | Leu | Leu | Ala | Leu |
| Leu 65 | Ser | Cys | Leu | Thr | Val 70 | Pro | Ala | Ser | Ala | Tyr 75 | Glu | Val | Arg | Asn | Val 80 |
| Ser | Gly | Met | Tyr | His 85 | Val | Thr | Asn | Asp | Cys 90 | Ser | Asn | Ser | Ser | Ile 95 | Val |
| Tyr | Glu | Ala | Ala 100 | Asp | Met | Ile | Met | His 105 | Thr | Pro | Gly | Cys | Val 110 | Pro | Cys |
| Val | Arg | Glu | Asn 115 | Asn | Ser | Ser | Arg | Cys 120 | Trp | Val | Ala | Leu 125 | Thr | Pro | Thr |
| Leu 130 | Ala | Ala | Arg | Asn | Ala | Ser | Val | Pro 135 | Thr | Thr | Thr | Ile 140 | Arg | Arg | His |
| Val 145 | Asp | Leu | Leu | Val | Gly 150 | Ala | Ala | Ala | Phe | Cys 155 | Ser | Ala | Met | Tyr | Val 160 |
| Gly | Asp | Leu | Cys 165 | Gly | Ser | Val | Phe | Leu 170 | Val | Ser | Gln | Leu | Phe | Thr 175 | Ile |
| Ser | Pro | Arg | Arg 180 | His | Glu | Thr | Val | Gln 185 | Asp | Cys | Asn | Cys | Ser | Ile | Tyr |
| Pro | Gly | His 195 | Ile | Thr | Gly | His | Arg | Met 200 | Ala | Trp | Asp | Met 205 | Met | Met | Asn |
| Trp 210 | Ser | Pro | Thr | Thr | Ala | Leu | Val | Val 215 | Ser | Gln | Leu 220 | Leu | Arg | Ile | Pro |
| Gln | Ala | Val | Val | Asp | Met | Val | Ala | Gly | Ala | His | Trp | Gly | Val | Leu | Ala |

(2) INFORMATION FOR SEO ID NO: 7:

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..630

(ix) FEATURE:

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(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..627
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | TTG | GGT | AAG | GTC | ATC | GAT | ACC | CTT | ACG | TGC | GGC | TTC | GCC | GAC | CTC | 48 |
| Met | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| ATG | GGG | TAC | ATT | CCG | CTC | GTC | GGC | GCC | CCC | CTA | GGG | GGT | GCT | GCC | AGA | 96 |
| Met | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu | Gly | Gly | Ala | Ala | Arg | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| GCC | CTG | GCG | CAT | GGC | GTC | CGG | GTT | CTG | GAA | GAC | GGC | GTG | AAC | TAT | GCA | 144 |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| ACA | GGG | AAT | TTG | CCT | GGT | TGC | TCT | TTC | TCT | ATC | TTC | CTC | TTG | GCT | TTA | 192 |
| Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| CTG | TCC | TGT | CTG | ACC | ATT | CCA | GCT | TCC | GCT | TAT | GAG | GTG | CGC | AAC | GTG | 240 |
| Leu | Ser | Cys | Leu | Thr | Ile | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| TCC | GGG | ATG | TAC | CAT | GTC | ACG | AAC | GAC | TGC | TCC | AAC | TCA | AGC | ATT | GTG | 288 |
| Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| TAT | GAG | GCA | GCG | GAC | ATG | ATC | ATG | CAC | ACC | CCC | GGG | TGC | GTG | CCC | TGC | 336 |
| Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr | Pro | Gly | Cys | Val | Pro | Cys | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |

| | |
|---|-----|
| GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG | 384 |
| Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr | |
| 115 120 125 | |
| CTC GCA GCT AGG AAC GCC AGC GTC CCC ACT ACG ACA ATA CGA CGC CAC | 432 |
| Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His | |
| 130 135 140 | |
| GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT TCC GCT ATG TAC GTG | 480 |
| Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val | |
| 145 150 155 160 | |
| GGG GAT CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC | 528 |
| Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile | |
| 165 170 175 | |
| TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT | 576 |
| Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr | |
| 180 185 190 | |
| CCC GGC CAC ATA ACA GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC | 624 |
| Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn | |
| 195 200 205 | |
| TGG TAATAG | 633 |
| Trp | |
| 210 | |

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 209 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Met | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu | Gly | Gly | Ala | Ala | Arg |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala |
| | 35 | | | | | | 40 | | | | | 45 | | | |
| Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu |
| | 50 | | | | | 55 | | | | 60 | | | | | |
| Leu | Ser | Cys | Leu | Thr | Ile | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val |
| | 65 | | | | 70 | | | | | 75 | | | | 80 | |
| Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val |
| | | | 85 | | | | | 90 | | | | | | 95 | |
| Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr | Pro | Gly | Cys | Val | Pro | Cys |
| | | | 100 | | | | | 105 | | | | | 110 | | |

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
 115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His
 130 135 140

Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val
 145 150 155 160

Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile
 165 170 175

Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr
 180 185 190

Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn
 195 200 205

Trp

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 483 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..480

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

| | |
|---|-----|
| ATG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCC CTG CTG TCC TGT | 48 |
| Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys | |
| 1 5 10 15 | |
| CTG ACC ATA CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG TCC GGG GTG | 96 |
| Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val | |
| 20 25 30 | |
| TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATA GTG TAT GAG GCA | 144 |
| Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala | |
| 35 40 45 | |
| GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG | 192 |
| Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu | |
| 50 55 60 | |

| | |
|--|-----|
| GGC AAC TCC TCC CGT TGC TGG GTG GCG CTC ACT CCC ACG CTC GCG GCC | 240 |
| Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala | |
| 65 70 75 80 | |
| AGG AAC GCC AGC GTC CCC ACA ACG ACA ATA CGA CGC CAC GTC GAT TTG | 288 |
| Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu | |
| 85 90 95 | |
| CTC GTT GGG GCT GCT GCT TTC TGT TCC GCT ATG TAC GTG GGG GAT CTC | 336 |
| Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu | |
| 100 105 110 | |
| TGC GGA TCT GTT TTC CTT GTT TCC CAG CTG TTC ACC TTC TCA CCT CGC | 384 |
| Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg | |
| 115 120 125 | |
| CGG CAT CAA ACA GTA CAG GAC TGC AAC TGC TCA ATC TAT CCC GGC CAT | 432 |
| Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His | |
| 130 135 140 | |
| GTA TCA GGT CAC CGC ATG GCT TGG GAT ATG ATG ATG AAC TGG TCC TAATAG | 483 |
| Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser | |
| 145 150 155 160 | |

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 159 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

| | |
|---|--|
| Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys | |
| 1 5 10 15 | |
| Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val | |
| 20 25 30 | |
| Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala | |
| 35 40 45 | |
| Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu | |
| 50 55 60 | |
| Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala | |
| 65 70 75 80 | |
| Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu | |
| 85 90 95 | |
| Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu | |
| 100 105 110 | |
| Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg | |
| 115 120 125 | |
| Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His | |

| | | |
|---|-----|-----|
| 130 | 135 | 140 |
| Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser | | |
| 145 | 150 | 155 |

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..477

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

| | |
|---|-----|
| ATG TCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCC CTG CTG TCC TGT | 48 |
| Met Ser Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys | |
| 1 5 10 15 | |
| CTG ACC ATA CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG TCC GGG GTG | 96 |
| Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val | |
| 20 25 30 | |
| TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATA GTG TAT GAG GCA | 144 |
| Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala | |
| 35 40 45 | |
| GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG | 192 |
| Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu | |
| 50 55 60 | |
| GGC AAC TCC TCC CGT TGC TGG GTG GCG CTC ACT CCC ACG CTC GCG GCC | 240 |
| Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala | |
| 65 70 75 80 | |
| AGG AAC GCC AGC GTC CCC ACA ACG ACA ATA CGA CGC CAC GTC GAT TTG | 288 |
| Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu | |
| 85 90 95 | |
| CTC GTT GGG GCT GCT GCT TTC TGT TCC GCT ATG TAC GTG GGG GAT CTC | 336 |
| Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu | |
| 100 105 110 | |
| TGC GGA TCT GTT TTC CTT GTT TCC CAG CTG TTC ACC TTC TCA CCT CGC | 384 |
| Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg | |

| | | | |
|---|-----|-----|-----|
| 115 | 120 | 125 | |
| CGG CAT CAA ACA GTA CAG GAC TGC AAC TGC TCA ATC TAT CCC GGC CAT | | | 432 |
| Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His | | | |
| 130 | 135 | 140 | |
| GTA TCA GGT CAC CGC ATG GCT TGG GAT ATG ATG ATG AAC TGG TAATAG | | | 480 |
| Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp | | | |
| 145 | 150 | 155 | |

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu | Leu | Ser | Cys |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Thr | Ile | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val | Ser | Gly | Val |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val | Tyr | Glu | Ala |
| | | 35 | | | | 40 | | | | | | 45 | | | |
| Ala | Asp | Met | Ile | Met | His | Thr | Pro | Gly | Cys | Val | Pro | Cys | Val | Arg | Glu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gly | Asn | Ser | Ser | Arg | Cys | Trp | Val | Ala | Leu | Thr | Pro | Thr | Leu | Ala | Ala |
| | 65 | | | | 70 | | | | | 75 | | | | 80 | |
| Arg | Asn | Ala | Ser | Val | Pro | Thr | Thr | Thr | Ile | Arg | Arg | His | Val | Asp | Leu |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Leu | Val | Gly | Ala | Ala | Ala | Phe | Cys | Ser | Ala | Met | Tyr | Val | Gly | Asp | Leu |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Cys | Gly | Ser | Val | Phe | Leu | Val | Ser | Gln | Leu | Phe | Thr | Phe | Ser | Pro | Arg |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Arg | His | Gln | Thr | Val | Gln | Asp | Cys | Asn | Cys | Ser | Ile | Tyr | Pro | Gly | His |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Val | Ser | Gly | His | Arg | Met | Ala | Trp | Asp | Met | Met | Met | Asn | Trp | | |
| 145 | | | | | 150 | | | | | 155 | | | | | |

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..633

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

| | |
|---|-----|
| ATG CTG GGT AAG GCC ATC GAT ACC CTT ACG TGC GGC TTC GCC GAC CTC | 48 |
| Met Leu Gly Lys Ala Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu | |
| 1 5 10 15 | |
| GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG | 96 |
| Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg | |
| 20 25 30 | |
| GCC CTG GCG CAT GGC GTC CGG GTT CTG GAA GAC GGC GTG AAC TAT GCA | 144 |
| Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala | |
| 35 40 45 | |
| ACA GGG AAT TTG CCT GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTA | 192 |
| Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu | |
| 50 55 60 | |
| CTG TCC TGT CTA ACC ATT CCA GCT TCC GCT TAC GAG GTG CGC AAC GTG | 240 |
| Leu Ser Cys Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val | |
| 65 70 75 80 | |
| TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG | 288 |
| Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val | |
| 85 90 95 | |
| TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC | 336 |
| Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys | |
| 100 105 110 | |
| GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG | 384 |
| Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr | |
| 115 120 125 | |
| CTC GCG GCT AGG AAC GCC AGC ATC CCC ACT ACA ACA ATA CGA CGC CAC | 432 |
| Leu Ala Ala Arg Asn Ala Ser Ile Pro Thr Thr Thr Ile Arg Arg His | |
| 130 135 140 | |
| GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT TCC GCT ATG TAC GTG | 480 |
| Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val | |
| 145 150 155 160 | |
| GGG GAT CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC | 528 |
| Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile | |
| 165 170 175 | |
| TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT | 576 |
| Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr | |

| | | | |
|---|-----|-----|-----|
| 180 | 185 | 190 | |
| CCC GGC CAC ATA ACG GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC | | | 624 |
| Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn | | | |
| 195 | 200 | 205 | |
| TGG TAC TAATAG | | | 640 |
| Trp Tyr | | | |
| 210 | | | |

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gly | Lys | Ala | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu | Gly | Gly | Ala | Ala | Arg |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala |
| | | 35 | | | | 40 | | | | | | 45 | | | |
| Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu |
| | | 50 | | | | 55 | | | | | 60 | | | | |
| Leu | Ser | Cys | Leu | Thr | Ile | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val |
| | 65 | | | | 70 | | | | | 75 | | | | | 80 |
| Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr | Pro | Gly | Cys | Val | Pro | Cys |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Val | Arg | Glu | Asn | Asn | Ser | Ser | Arg | Cys | Trp | Val | Ala | Leu | Thr | Pro | Thr |
| | | | 115 | | | | 120 | | | | | 125 | | | |
| Leu | Ala | Ala | Arg | Asn | Ala | Ser | Ile | Pro | Thr | Thr | Thr | Ile | Arg | Arg | His |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Val | Asp | Leu | Leu | Val | Gly | Ala | Ala | Ala | Phe | Cys | Ser | Ala | Met | Tyr | Val |
| | 145 | | | | 150 | | | | | 155 | | | | | 160 |
| Gly | Asp | Leu | Cys | Gly | Ser | Val | Phe | Leu | Val | Ser | Gln | Leu | Phe | Thr | Ile |
| | | | 165 | | | | | 170 | | | | | 175 | | |
| Ser | Pro | Arg | Arg | His | Glu | Thr | Val | Gln | Asp | Cys | Asn | Cys | Ser | Ile | Tyr |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Pro | Gly | His | Ile | Thr | Gly | His | Arg | Met | Ala | Trp | Asp | Met | Met | Met | Asn |
| | | 195 | | | | | 200 | | | | | 205 | | | |

Trp Tyr
210

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ATGCCCGGTT GCTCTTCTC TATCTT

26

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ATGTTGGGTA AGGTCATCGA TACCCT

26

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CTATTAGGAC CAGTTCATCA TCATATCCCA

30

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CTATTACCAG TTCATCATCA TATCCCA

27

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATACGACGCC ACGTCGATTC CCAGCTGTTC ACCATC

36

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GATGGTGAAC AGCTGGGAAT CGACGTGGCG TCGTAT

36

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 723 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..720

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

| | |
|---|-----|
| ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC | 48 |
| Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu | |
| 1 5 10 15 | |
| GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG | 96 |
| Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg | |
| 20 25 30 | |
| GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA | 144 |
| Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala | |
| 35 40 45 | |
| ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG | 192 |
| Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu | |
| 50 55 60 | |
| CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG | 240 |
| Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val | |
| 65 70 75 80 | |
| TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG | 288 |
| Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val | |
| 85 90 95 | |
| TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC | 336 |
| Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys | |
| 100 105 110 | |
| GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG | 384 |
| Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr | |
| 115 120 125 | |
| CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC | 432 |
| Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His | |
| 130 135 140 | |
| GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG | 480 |
| Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val | |

| | | | | | | | |
|--|--|-----|--|-----|--|-----|-----|
| 145 | | 150 | | 155 | | 160 | |
| CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT | | | | | | | 528 |
| Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg | | | | | | | |
| | | 165 | | 170 | | 175 | |
| ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG | | | | | | | 576 |
| Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val | | | | | | | |
| | | 180 | | 185 | | 190 | |
| GTA TCG CAG CTG CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG | | | | | | | 624 |
| Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala | | | | | | | |
| | | 195 | | 200 | | 205 | |
| GGG GCC CAT TGG GGA GTC CTG GCG GGT CTC GCC TAC TAT TCC ATG GTG | | | | | | | 672 |
| Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val | | | | | | | |
| | | 210 | | 215 | | 220 | |
| GGG AAC TGG GCT AAG GTT TTG ATT GTG ATG CTA CTC TTT GCT CCC TAATAG | | | | | | | 723 |
| Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu Leu Phe Ala Pro | | | | | | | |
| | | 225 | | 230 | | 235 | 240 |

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 239 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu | Gly | Gly | Ala | Ala | Arg |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala |
| | | 35 | | | | 40 | | | | | | 45 | | | |
| Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu |
| | 50 | | | | 55 | | | | | 60 | | | | | |
| Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val |
| | 65 | | | | 70 | | | | | 75 | | | | 80 | |
| Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val |
| | | | 85 | | | | | 90 | | | | | | 95 | |
| Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr | Pro | Gly | Cys | Val | Pro | Cys |
| | | 100 | | | | | 105 | | | | | | 110 | | |
| Val | Arg | Glu | Asn | Asn | Ser | Ser | Arg | Cys | Trp | Val | Ala | Leu | Thr | Pro | Thr |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Leu | Ala | Ala | Arg | Asn | Ala | Ser | Val | Pro | Thr | Thr | Thr | Ile | Arg | Arg | His |
| | 130 | | | | | 135 | | | | | | 140 | | | |
| Val | Asp | Ser | Gln | Leu | Phe | Thr | Ile | Ser | Pro | Arg | Arg | His | Glu | Thr | Val |

| | | | | | | |
|---|-----|-----|--|-----|--|-----|
| 145 | | 150 | | 155 | | 160 |
| Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg | | | | | | |
| | 165 | | | 170 | | 175 |
| Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val | | | | | | |
| | 180 | | | 185 | | 190 |
| Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala | | | | | | |
| | 195 | | | 200 | | 205 |
| Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val | | | | | | |
| | 210 | | | 215 | | 220 |
| Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu Leu Phe Ala Pro | | | | | | |
| | 225 | | | 230 | | 235 |

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 561 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..558

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

| | |
|---|-----|
| ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC | 48 |
| Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu | |
| 1 5 10 15 | |
| GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG | 96 |
| Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg | |
| 20 25 30 | |
| GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA | 144 |
| Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala | |
| 35 40 45 | |
| ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG | 192 |
| Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu | |
| 50 55 60 | |
| CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG | 240 |
| Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val | |

| 65 | 70 | 75 | 80 | |
|---|-----|-----|-----|-----|
| TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG | | | | 288 |
| Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val | 85 | 90 | 95 | |
| TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC | | | | 336 |
| Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys | 100 | 105 | 110 | |
| GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG | | | | 384 |
| Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr | 115 | 120 | 125 | |
| CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC | | | | 432 |
| Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His | 130 | 135 | 140 | |
| GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG | | | | 480 |
| Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val | 145 | 150 | 155 | 160 |
| CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT | | | | 528 |
| Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg | 165 | 170 | 175 | |
| ATG GCT TGG GAT ATG ATG ATG AAC TGG TAATAG | | | | 561 |
| Met Ala Trp Asp Met Met Met Asn Trp | 180 | 185 | | |

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 185 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu | Gly | Gly | Ala | Ala | Arg |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu |
| | | 50 | | | | 55 | | | | | 60 | | | | |
| Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr | Pro | Gly | Cys | Val | Pro | Cys |
| | | | 100 | | | | | 105 | | | | | 110 | | |

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
 115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His
 130 135 140

Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val
 145 150 155 160

Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg
 165 170 175

Met Ala Trp Asp Met Met Met Asn Trp
 180 185

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 606 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..603

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

| | |
|---|-----|
| ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC | 48 |
| Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu | |
| 1 5 10 15 | |
| GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG | 96 |
| Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg | |
| 20 25 30 | |
| GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA | 144 |
| Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala | |
| 35 40 45 | |
| ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG | 192 |
| Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu | |
| 50 55 60 | |
| CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG | 240 |
| Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val | |
| 65 70 75 80 | |

TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG 288
 Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val
 85 95

TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC 336
 Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
 100 105 110

GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG 384
 Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
 115 120 125

CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC 432
 Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His
 130 135 140

GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG 480
 Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val
 145 150 155 160

CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT 528
 Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg
 165 170 175

ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG 576
 Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val
 180 185 190

GTA TCG CAG CTG CTC CGG ATC CTC TAATAG 606
 Val Ser Gln Leu Leu Arg Ile Leu
 195 200

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu
 1 5 10 15

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg
 20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala
 35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu
 50 55 60

Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val
 65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val
 85 90 95

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
 100 105 110
 Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
 115 120 125
 Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His
 130 135 140
 Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val
 145 150 155 160
 Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg
 165 170 175
 Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val
 180 185 190
 Val Ser Gln Leu Leu Arg Ile Leu
 195 200

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 636 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..633

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | TTG | GGT | AAG | GTC | ATC | GAT | ACC | CTT | ACA | TGC | GGC | TTC | GCC | GAC | CTC | 48 |
| Met | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| GTG | GGG | TAC | ATT | CCG | CTC | GTC | GGC | GCC | CCC | CTA | GGG | GGC | GCT | GCC | AGG | 96 |
| Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu | Gly | Gly | Ala | Ala | Arg | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| GCC | CTG | GCG | CAT | GGC | GTC | CGG | GTT | CTG | GAG | GAC | GGC | GTG | AAC | TAT | GCA | 144 |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala | |
| | | | 35 | | | | 40 | | | | | 45 | | | | |
| ACA | GGG | AAT | TTG | CCC | GGT | TGC | TCT | TTC | TCT | ATC | TTC | CTC | TTG | GCT | TTG | 192 |

| | | | | | | | | | | | | | | | | | |
|-----|-----|--------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu | | |
| 50 | | | | | | 55 | | | | | 60 | | | | | | |
| CTG | TCC | TGT | CTG | ACC | GTT | CCA | GCT | TCC | GCT | TAT | GAA | GTG | CGC | AAC | GTG | 240 | |
| Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val | 80 | |
| 65 | | | | | 70 | | | | | 75 | | | | | | | |
| TCC | GGG | ATG | TAC | CAT | GTC | ACG | AAC | GAC | TGC | TCC | AAC | TCA | AGC | ATT | GTG | 288 | |
| Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val | 95 | |
| | | | | 85 | | | | | 90 | | | | | | | | |
| TAT | GAG | GCA | GCG | GAC | ATG | ATC | ATG | CAC | ACC | CCC | GGG | TGC | GTG | CCC | TGC | 336 | |
| Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr | Pro | Gly | Cys | Val | Pro | Cys | 110 | |
| | | | 100 | | | | | 105 | | | | | | | | | |
| GTT | CGG | GAG | AAC | AAC | TCT | TCC | CGC | TGC | TGG | GTA | GCG | CTC | ACC | CCC | ACG | 384 | |
| Val | Arg | Glu | Asn | Asn | Ser | Ser | Arg | Cys | Trp | Val | Ala | Leu | Thr | Pro | Thr | 125 | |
| | | 115 | | | | | 120 | | | | | | | | | | |
| CTC | GCA | GCT | AGG | AAC | GCC | AGC | GTC | CCC | ACC | ACG | ACA | ATA | CGA | CGC | CAC | 432 | |
| Leu | Ala | Ala | Arg | Asn | Ala | Ser | Val | Pro | Thr | Thr | Thr | Ile | Arg | Arg | His | 140 | |
| | | | 130 | | | | 135 | | | | | | | | | | |
| GTC | GAT | TCC | CAG | CTG | TTC | ACC | ATC | TCG | CCT | CGC | CGG | CAT | GAG | ACG | GTG | 480 | |
| Val | Asp | Ser | Gln | Leu | Phe | Thr | Ile | Ser | Pro | Arg | Arg | His | Glu | Thr | Val | 160 | |
| | | | | | 150 | | | | | 155 | | | | | | | |
| CAG | GAC | TGC | AAT | TGC | TCA | ATC | TAT | CCC | GGC | CAC | ATA | ACG | GGT | CAC | CGT | 528 | |
| Gln | Asp | Cys | Asn | Cys | Ser | Ile | Tyr | Pro | Gly | His | Ile | Thr | Gly | His | Arg | 175 | |
| | | | | 165 | | | | | 170 | | | | | | | | |
| ATG | GCT | TGG | GAT | ATG | ATG | ATG | AAC | TGG | TCG | CCT | ACA | ACG | GCC | CTG | GTG | 576 | |
| Met | Ala | Trp | Asp | Met | Met | Met | Asn | Trp | Ser | Pro | Thr | Thr | Ala | Leu | Val | 190 | |
| | | | 180 | | | | | 185 | | | | | | | | | |
| GTA | TCG | CAG | CTG | CTC | CGG | ATC | GTG | ATC | GAG | GGC | AGA | CAC | CAT | CAC | CAC | 624 | |
| Val | Ser | Gln | Leu | Leu | Arg | Ile | Val | Ile | Glu | Gly | Arg | His | His | His | His | 205 | |
| | | | 195 | | | | 200 | | | | | | | | | | |
| CAT | CAC | TAATAG | | | | | | | | | | | | | | 636 | |
| His | His | | | | | | | | | | | | | | | | |
| | | 210 | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 210 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu | Gly | Gly | Ala | Ala | Arg |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala |

35 40 45
 Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu
 50 55 60
 Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val
 65 70 75 80
 Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val
 85 90 95
 Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
 100 105 110
 Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
 115 120 125
 Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His
 130 135 140
 Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val
 145 150 155 160
 Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg
 165 170 175
 Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val
 180 185 190
 Val Ser Gln Leu Leu Arg Ile Val Ile Glu Gly Arg His His His His
 195 200 205
 His His
 210

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..627

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ATG GGT AAG GTC ATC GAT ACC CTT ACG TGC GGA TTC GCC GAT CTC ATG

| | | | | | | | | | | | | | | | | |
|--------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu | Met | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| GGG | TAC | ATC | CCG | CTC | GTC | GGC | GCT | CCC | GTA | GGA | GGC | GTC | GCA | AGA | GCC | 96 |
| Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Val | Gly | Gly | Val | Ala | Arg | Ala | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| CTT | GCG | CAT | GGC | GTG | AGG | GCC | CTT | GAA | GAC | GGG | ATA | AAT | TTC | GCA | ACA | 144 |
| Leu | Ala | His | Gly | Val | Arg | Ala | Leu | Glu | Asp | Gly | Ile | Asn | Phe | Ala | Thr | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| GGG | AAT | TTG | CCC | GGT | TGC | TCC | TTT | TCT | ATT | TTC | CTT | CTC | GCT | CTG | TTC | 192 |
| Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu | Phe | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| TCT | TGC | TTA | ATT | CAT | CCA | GCA | GCT | AGT | CTA | GAG | TGG | CGG | AAT | ACG | TCT | 240 |
| Ser | Cys | Leu | Ile | His | Pro | Ala | Ala | Ser | Leu | Glu | Trp | Arg | Asn | Thr | Ser | |
| | 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| GGC | CTC | TAT | GTC | CTT | ACC | AAC | GAC | TGT | TCC | AAT | AGC | AGT | ATT | GTG | TAC | 288 |
| Gly | Leu | Tyr | Val | Leu | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val | Tyr | |
| | | | 85 | | | | | | 90 | | | | | 95 | | |
| GAG | GCC | GAT | GAC | GTT | ATT | CTG | CAC | ACA | CCC | GGC | TGC | ATA | CCT | TGT | GTC | 336 |
| Glu | Ala | Asp | Asp | Val | Ile | Leu | His | Thr | Pro | Gly | Cys | Ile | Pro | Cys | Val | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| CAG | GAC | GGC | AAT | ACA | TCC | ACG | TGC | TGG | ACC | CCA | GTG | ACA | CCT | ACA | GTG | 384 |
| Gln | Asp | Gly | Asn | Thr | Ser | Thr | Cys | Trp | Thr | Pro | Val | Thr | Pro | Thr | Val | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| GCA | GTC | AAG | TAC | GTC | GGA | GCA | ACC | ACC | GCT | TCG | ATA | CGC | AGT | CAT | GTG | 432 |
| Ala | Val | Lys | Tyr | Val | Gly | Ala | Thr | Thr | Ala | Ser | Ile | Arg | Ser | His | Val | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| GAC | CTA | TTA | GTG | GGC | GCG | GCC | ACG | ATG | TGC | TCT | GCG | CTC | TAC | GTG | GGT | 480 |
| Asp | Leu | Leu | Val | Gly | Ala | Ala | Thr | Met | Cys | Ser | Ala | Leu | Tyr | Val | Gly | |
| | 145 | | | | 150 | | | | 155 | | | | | | 160 | |
| GAC | ATG | TGT | GGG | GCT | GTC | TTC | CTC | GTG | GGA | CAA | GCC | TTC | ACG | TTC | AGA | 528 |
| Asp | Met | Cys | Gly | Ala | Val | Phe | Leu | Val | Gly | Gln | Ala | Phe | Thr | Phe | Arg | |
| | | | 165 | | | | | | 170 | | | | | 175 | | |
| CCT | CGT | CGC | CAT | CAA | ACG | GTC | CAG | ACC | TGT | AAC | TGC | TCG | CTG | TAC | CCA | 576 |
| Pro | Arg | Arg | His | Gln | Thr | Val | Gln | Thr | Cys | Asn | Cys | Ser | Leu | Tyr | Pro | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| GGC | CAT | CTT | TCA | GGA | CAT | CGA | ATG | GCT | TGG | GAT | ATG | ATG | ATG | AAC | TGG | 624 |
| Gly | His | Leu | Ser | Gly | His | Arg | Met | Ala | Trp | Asp | Met | Met | Met | Asn | Trp | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| TAATAG | | | | | | | | | | | | | | | | 634 |

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 208 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met
 1 5 10 15
 Gly Tyr Ile Pro Leu Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala
 20 25 30
 Leu Ala His Gly Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr
 35 40 45
 Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe
 50 55 60
 Ser Cys Leu Ile His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser
 65 70 75 80
 Gly Leu Tyr Val Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr
 85 90 95
 Glu Ala Asp Asp Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val
 100 105 110
 Gln Asp Gly Asn Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val
 115 120 125
 Ala Val Lys Tyr Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val
 130 135 140
 Asp Leu Leu Val Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly
 145 150 155 160
 Asp Met Cys Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg
 165 170 175
 Pro Arg Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro
 180 185 190
 Gly His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 195 200 205

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..627

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

| | |
|---|-----|
| ATG GGT AAG GTC ATC GAT ACC CTA ACG TGC GGA TTC GCC GAT CTC ATG | 48 |
| Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met | |
| 1 5 10 15 | |
| GGG TAT ATC CCG CTC GTA GGC GGC CCC ATT GGG GGC GTC GCA AGG GCT | 96 |
| Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile Gly Gly Val Ala Arg Ala | |
| 20 25 30 | |
| CTC GCA CAC GGT GTG AGG GTC CTT GAG GAC GGG GTA AAC TAT GCA ACA | 144 |
| Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr | |
| 35 40 45 | |
| GGG AAT TTA CCC GGT TGC TCT TTC TCT ATC TTT ATT CTT GCT CTT CTC | 192 |
| Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu | |
| 50 55 60 | |
| TCG TGT CTG ACC GTT CCG GCC TCT GCA GTT CCC TAC CGA AAT GCC TCT | 240 |
| Ser Cys Leu Thr Val Pro Ala Ser Ala Val Pro Tyr Arg Asn Ala Ser | |
| 65 70 75 80 | |
| GGG ATT TAT CAT GTT ACC AAT GAT TGC CCA AAC TCT TCC ATA GTC TAT | 288 |
| Gly Ile Tyr His Val Thr Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr | |
| 85 90 95 | |
| GAG GCA GAT AAC CTG ATC CTA CAC GCA CCT GGT TGC GTG CCT TGT GTC | 336 |
| Glu Ala Asp Asn Leu Ile Leu His Ala Pro Gly Cys Val Pro Cys Val | |
| 100 105 110 | |
| ATG ACA GGT AAT GTG AGT AGA TGC TGG GTC CAA ATT ACC CCT ACA CTG | 384 |
| Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile Thr Pro Thr Leu | |
| 115 120 125 | |
| TCA GCC CCG AGC CTC GGA GCA GTC ACG GCT CCT CTT CGG AGA GCC GTT | 432 |
| Ser Ala Pro Ser Leu Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val | |
| 130 135 140 | |
| GAC TAC CTA GCG GGA GGG GCT GCC CTC TGC TCC GCG TTA TAC GTA GGA | 480 |
| Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly | |
| 145 150 155 160 | |
| GAC GCG TGT GGG GCA CTA TTC TTG GTA GGC CAA ATG TTC ACC TAT AGG | 528 |
| Asp Ala Cys Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg | |
| 165 170 175 | |
| CCT CGC CAG CAC GCT ACG GTG CAG AAC TGC AAC TGT TCC ATT TAC AGT | 576 |
| Pro Arg Gln His Ala Thr Val Gln Asn Cys Asn Cys Ser Ile Tyr Ser | |
| 180 185 190 | |
| GGC CAT GTT ACC GGC CAC CGG ATG GCA TGG GAT ATG ATG ATG AAC TGG | 624 |
| Gly His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp | |
| 195 200 205 | |

TAATAG

630

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met
 1 5 10 15

Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile Gly Gly Val Ala Arg Ala
 20 25 30

Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr
 35 40 45

Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
 50 55 60

Ser Cys Leu Thr Val Pro Ala Ser Ala Val Pro Tyr Arg Asn Ala Ser
 65 70 75 80

Gly Ile Tyr His Val Thr Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr
 85 90 95

Glu Ala Asp Asn Leu Ile Leu His Ala Pro Gly Cys Val Pro Cys Val
 100 105 110

Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile Thr Pro Thr Leu
 115 120 125

Ser Ala Pro Ser Leu Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val
 130 135 140

Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly
 145 150 155 160

Asp Ala Cys Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg
 165 170 175

Pro Arg Gln His Ala Thr Val Gln Asn Cys Asn Cys Ser Ile Tyr Ser
 180 185 190

Gly His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 195 200 205

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:
TGGGATATGA TGATGAACTG GTC

23

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:
CTATTATGGT GGTAAGCCAC AGAGCAGGAG

30

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1476 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1473

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG GTA TCG

48

| | | | | | | | | | | | | | | | | |
|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| Trp 1 | Asp | Met | Met | Met 5 | Asn | Trp | Ser | Pro | Thr 10 | Ala | Leu | Val 15 | Ser | | | |
| CAG Gln | CTG Leu | CTC Leu | CGG Arg 20 | ATC Ile | CCA Pro | CAA Gln | GCT Ala | GTC Val 25 | GTG Val | GAC Asp | ATG Met | GTG Val 30 | GCG Ala 30 | GGG Gly 30 | GCC Ala 30 | 96 |
| CAT His | TGG Trp | GGA Gly 35 | GTC Val | CTG Leu | GCG Ala | GGC Gly | CTC Leu 40 | GCC Ala | TAC Tyr | TAT Tyr | TCC Ser | ATG Met 45 | GTG Val | GGG Gly | AAC Asn | 144 |
| TGG Trp 50 | GCT Ala | AAG Lys | GTT Val | TTG Leu | GTT Val | GTG Val 55 | ATG Met | CTA Leu | CTC Leu | TTT Phe | GCC Ala 60 | GGC Gly | GTC Val | GAC Asp | GGG Gly | 192 |
| CAT His 65 | ACC Thr | CGC Arg | GTG Val | TCA Ser | GGA Gly 70 | GGG Gly | GCA Ala | GCA Ala | GCC Ala | TCC Ser 75 | GAT Asp | ACC Thr | AGG Arg | GGC Gly | CTT Leu 80 | 240 |
| GTG Val | TCC Ser | CTC Leu | TTT Phe | AGC Ser 85 | CCC Pro | GGG Gly | TCG Ser | GCT Ala | CAG Gln 90 | AAA Lys | ATC Ile | CAG Gln | CTC Leu | GTA Val 95 | AAC Asn | 288 |
| ACC Thr | AAC Asn | GGC Gly | AGT Ser 100 | TGG Trp | CAC His | ATC Ile | AAC Asn | AGG Arg 105 | ACT Thr | GCC Ala | CTG Leu | AAC Asn | TGC Cys 110 | AAC Asn | GAC Asp | 336 |
| TCC Ser | CTC Leu | CAA Gln 115 | ACA Thr | GGG Gly | TTC Phe | TTT Phe | GCC Ala 120 | GCA Ala | CTA Leu | TTC Phe | TAC Tyr | AAA Lys 125 | CAC His | AAA Lys | TTC Phe | 384 |
| AAC Asn 130 | TCG Ser | TCT Ser | GGA Gly | TGC Cys | CCA Pro | GAG Glu 135 | CGC Arg | TTG Leu | GCC Ala | AGC Ser | TGT Cys 140 | CGC Arg | TCC Ser | ATC Ile | GAC Asp | 432 |
| AAG Lys 145 | TTC Phe | GCT Ala | CAG Gln | GGG Gly | TGG Trp 150 | GGT Gly | CCC Pro | CTC Leu | ACT Thr | TAC Tyr 155 | ACT Thr | GAG Glu | CCT Pro | AAC Asn | AGC Ser 160 | 480 |
| TCG Ser | GAC Asp | CAG Gln | AGG Arg | CCC Pro 165 | TAC Tyr | TGC Cys | TGG Trp | CAC His | TAC Tyr 170 | GCG Ala | CCT Pro | CGA Arg | CCG Pro | TGT Cys 175 | GGT Gly | 528 |
| ATT Ile | GTA Val | CCC Pro | GCG Ala 180 | TCT Ser | CAG Gln | GTG Val | TGC Cys | GGT Gly 185 | CCA Pro | GTG Val | TAT Tyr | TGC Cys | TTC Phe 190 | ACC Thr | CCG Pro | 576 |
| AGC Ser | CCT Pro | GTT Val 195 | GTG Val | GTG Val | GGG Gly | ACG Thr | ACC Thr 200 | GAT Asp | CGG Arg | TTT Phe | GGT Gly | GTC Val 205 | CCC Pro | ACG Thr | TAT Tyr | 624 |
| AAC Asn 210 | TGG Trp | GGG Gly | GCG Ala | AAC Asn | GAC Asp | TCG Ser 215 | GAT Asp | GTG Val | CTG Leu | ATT Ile | CTC Leu 220 | AAC Asn | AAC Asn | ACG Thr | CGG Arg | 672 |
| CCG Pro 225 | CCG Pro | CGA Arg | GGC Gly | AAC Asn | TGG Trp 230 | TTC Phe | GGC Gly | TGT Cys | ACA Thr | TGG Trp 235 | ATG Met | AAT Asn | GGC Gly | ACT Thr | GGG Gly 240 | 720 |
| TTC Phe | ACC Thr | AAG Lys | ACG Thr | TGT Cys 245 | GGG Gly | GGC Gly | CCC Pro | CCG Pro | TGC Cys 250 | AAC Asn | ATC Ile | GGG Gly | GGG Gly | GCC Ala 255 | GGC Gly | 768 |

| | | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| AAC Asn | AAC Asn | ACC Thr | TTG Leu | ACC Thr | TGC Cys | CCC Pro | ACT Thr | GAC Asp | TGT Cys | TTT Phe | CGG Arg | AAG Lys | CAC His | CCC Pro | GAG Glu | 816 |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| GCC Ala | ACC Thr | TAC Tyr | GCC Ala | AGA Arg | TGC Cys | GGT Gly | TCT Ser | GGG Gly | CCC Pro | TGG Trp | CTG Leu | ACA Thr | CCT Pro | AGG Arg | TGT Cys | 864 |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| ATG Met | GTT Val | CAT His | TAC Tyr | CCA Pro | TAT Tyr | AGG Arg | CTC Leu | TGG Trp | CAC His | TAC Tyr | CCC Pro | TGC Cys | ACT Thr | GTC Val | AAC Asn | 912 |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| TTC Phe | ACC Thr | ATC Ile | TTC Phe | AAG Lys | GTT Val | AGG Arg | ATG Met | TAC Tyr | GTG Val | GGG Gly | GGC Val | GTG Glu | GAG His | CAC His | AGG Arg | 960 |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| TTC Phe | GAA Glu | GCC Ala | GCA Ala | TGC Cys | AAT Asn | TGG Trp | ACT Thr | CGA Arg | GGA Gly | GAG Glu | CGT Arg | TGT Cys | GAC Asp | TTG Leu | GAG Glu | 1008 |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| GAC Asp | AGG Arg | GAT Asp | AGA Arg | TCA Ser | GAG Glu | CTT Leu | AGC Ser | CCG Pro | CTG Leu | CTG Leu | CTG Leu | TCT Ser | ACA Thr | ACA Thr | GAG Glu | 1056 |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| TGG Trp | CAG Gln | ATA Ile | CTG Leu | CCC Pro | TGT Cys | TCC Ser | TTC Phe | ACC Thr | ACC Thr | CTG Leu | CCG Pro | GCC Ala | CTA Leu | TCC Ser | ACC Thr | 1104 |
| | | 355 | | | | | 360 | | | | | 365 | | | | |
| GGC Gly | CTG Leu | ATC Ile | CAC His | CTC Leu | CAT His | CAG Gln | AAC Asn | ATC Ile | GTG Val | GAC Asp | GTG Val | CAA Gln | TAC Tyr | CTG Leu | TAC Tyr | 1152 |
| | 370 | | | | | 375 | | | | | 380 | | | | | |
| GGT Gly | GTA Val | GGG Gly | TCG Ser | GCG Ala | GTT Val | GTC Val | TCC Ser | CTT Leu | GTC Val | ATC Ile | AAA Lys | TGG Trp | GAG Glu | TAT Tyr | GTC Val | 1200 |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| CTG Leu | TTG Leu | CTC Leu | TTC Phe | CTT Leu | CTC Leu | CTG Leu | GCA Ala | GAC Asp | GCG Ala | CGC Arg | ATC Ile | TGC Cys | GCC Ala | TGC Cys | TTA Leu | 1248 |
| | | | | 405 | | | | 410 | | | | | 415 | | | |
| TGG Trp | ATG Met | ATG Met | CTG Leu | CTG Leu | ATA Ile | GCT Ala | CAA Gln | GCT Ala | GAG Glu | GCC Ala | GCC Ala | TTA Leu | GAG Glu | AAC Asn | CTG Leu | 1296 |
| | | | 420 | | | | 425 | | | | | 430 | | | | |
| GTG Val | GTC Val | CTC Leu | AAT Asn | GCG Ala | GCG Ala | GCC Ala | GTG Val | GCC Ala | GGG Gly | GCG Ala | CAT His | GGC Gly | ACT Thr | CTT Leu | TCC Ser | 1344 |
| | | 435 | | | | | 440 | | | | | 445 | | | | |
| TTC Phe | CTT Leu | GTG Val | TTC Phe | TTC Phe | TGT Cys | GCT Ala | GCC Ala | TGG Trp | TAC Tyr | ATC Ile | AAG Lys | GGC Gly | AGG Arg | CTG Leu | GTC Val | 1392 |
| | 450 | | | | | 455 | | | | | 460 | | | | | |
| CCT Pro | GGT Gly | GCG Ala | GCA Ala | TAC Tyr | GCC Ala | TTC Phe | TAT Tyr | GGC Gly | GTG Val | TGG Trp | CCG Pro | CTG Leu | CTC Leu | CTG Leu | CTT Leu | 1440 |
| 465 | | | | | 470 | | | | 475 | | | | | | 480 | |
| CTG Leu | CTG Leu | GCC Ala | TTA Leu | CCA Pro | CCA Pro | CGA Arg | GCT Ala | TAT Tyr | GCC Ala | TAGTAA | | | | | | 1476 |
| | | | | 485 | | | | | 490 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val Val Ser
 1           5           10           15
Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala
      20           25           30
His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn
      35           40           45
Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly
      50           55           60
His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu
      65           70           75           80
Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn
      85           90           95
Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp
      100          105          110
Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe
      115          120          125
Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp
      130          135          140
Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser
      145          150          155          160
Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly
      165          170          175
Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro
      180          185          190
Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr
      195          200          205
Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg
      210          215          220
Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly
      225          230          235          240
Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly
      245          250          255
Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu
      260          265          270
Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys

```

| 275 | 280 | 285 |
|---|---|---------------------|
| Met Val His Tyr Pro Tyr | Arg Leu Trp His Tyr | Pro Cys Thr Val Asn |
| 290 | 295 | 300 |
| Phe Thr Ile Phe Lys Val | Arg Met Tyr Val Gly Gly Val Glu His Arg | |
| 305 | 310 | 315 320 |
| Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu | | |
| | 325 | 330 335 |
| Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu | | |
| | 340 | 345 350 |
| Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr | | |
| | 355 | 360 365 |
| Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr | | |
| | 370 | 375 380 |
| Gly Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val | | |
| | 385 | 390 395 400 |
| Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu | | |
| | 405 | 410 415 |
| Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu | | |
| | 420 | 425 430 |
| Val Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser | | |
| | 435 | 440 445 |
| Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val | | |
| | 450 | 455 460 |
| Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu | | |
| | 465 | 470 475 480 |
| Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala | | |
| | 485 | 490 |

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1021 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..1018

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide

(B) LOCATION: 2..1015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

| | |
|---|-----|
| G ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA | 46 |
| Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly | |
| 1 5 10 15 | |
| GTC CTG GCG GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG | 94 |
| Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys | |
| 20 25 30 | |
| GTT TTG GTT GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT ACC CGC | 142 |
| Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg | |
| 35 40 45 | |
| GTG TCA GGA GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT GTG TCC CTC | 190 |
| Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu | |
| 50 55 60 | |
| TTT AGC CCC GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC AAC GGC | 238 |
| Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly | |
| 65 70 75 | |
| AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC CTC CAA | 286 |
| Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln | |
| 80 85 90 95 | |
| ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC TCG TCT | 334 |
| Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser | |
| 100 105 110 | |
| GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG TTC GCT | 382 |
| Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala | |
| 115 120 125 | |
| CAG GGG TGG GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG GAC CAG | 430 |
| Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln | |
| 130 135 140 | |
| AGG CCC TAC TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT GTA CCC | 478 |
| Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro | |
| 145 150 155 | |
| GCG TCT CAG GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC CCT GTT | 526 |
| Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val | |
| 160 165 170 175 | |
| GTG GTG GGG ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC TGG GGG | 574 |
| Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly | |
| 180 185 190 | |
| GCG AAC GAC TCG GAT GTG CTG ATT CTC AAC AAC ACG CGG CCG CCG CGA | 622 |
| Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg | |
| 195 200 205 | |
| GGC AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG | 670 |
| Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys | |
| 210 215 220 | |
| ACG TGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC | 718 |
| Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr | |

| 225 | 230 | 235 | |
|---|-----|-----|------|
| TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC ACC TAC Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr 240 245 250 255 | | | 766 |
| GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG GTT CAT Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His 260 265 270 | | | 814 |
| TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC ACC ATC Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile 275 280 285 | | | 862 |
| TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC GAA GCC Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala 290 295 300 | | | 910 |
| GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC AGG GAT Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp 305 310 315 | | | 958 |
| AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GAG TGG CAG AGT Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ser 320 325 330 335 | | | 1006 |
| GGC AGA GCT TAATTA Gly Arg Ala | | | 1021 |

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 338 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Ile | Pro | Gln | Ala | Val | Val | Asp | Met | Val | Ala | Gly | Ala | His | Trp | Gly | Val | 1 | 5 | 10 | 15 |
| Leu | Ala | Gly | Leu | Ala | Tyr | Tyr | Ser | Met | Val | Gly | Asn | Trp | Ala | Lys | Val | 20 | 25 | 30 | |
| Leu | Val | Val | Met | Leu | Leu | Phe | Ala | Gly | Val | Asp | Gly | His | Thr | Arg | Val | 35 | 40 | 45 | |
| Ser | Gly | Gly | Ala | Ala | Ala | Ser | Asp | Thr | Arg | Gly | Leu | Val | Ser | Leu | Phe | 50 | 55 | 60 | |
| Ser | Pro | Gly | Ser | Ala | Gln | Lys | Ile | Gln | Leu | Val | Asn | Thr | Asn | Gly | Ser | 65 | 70 | 75 | 80 |
| Trp | His | Ile | Asn | Arg | Thr | Ala | Leu | Asn | Cys | Asn | Asp | Ser | Leu | Gln | Thr | 85 | 90 | 95 | |
| Gly | Phe | Phe | Ala | Ala | Leu | Phe | Tyr | Lys | His | Lys | Phe | Asn | Ser | Ser | Gly | 100 | 105 | 110 | |

Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln
 115 120 125
 Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg
 130 135 140
 Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala
 145 150 155 160
 Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val
 165 170 175
 Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala
 180 185 190
 Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly
 195 200 205
 Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr
 210 215 220
 Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu
 225 230 235 240
 Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala
 245 250 255
 Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr
 260 265 270
 Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe
 275 280 285
 Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala
 290 295 300
 Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg
 305 310 315 320
 Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ser Gly
 325 330 335
 Arg Ala

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1034 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 2..1032

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 2..1029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

| | |
|---|-----|
| G ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA | 46 |
| Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly | |
| 1 5 10 15 | |
| GTC CTG GCG GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG | 94 |
| Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys | |
| 20 25 30 | |
| GTT TTG GTT GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT ACC CGC | 142 |
| Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg | |
| 35 40 45 | |
| GTG TCA GGA GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT GTG TCC CTC | 190 |
| Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu | |
| 50 55 60 | |
| TTT AGC CCC GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC AAC GGC | 238 |
| Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly | |
| 65 70 75 | |
| AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC CTC CAA | 286 |
| Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln | |
| 80 85 90 95 | |
| ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC TCG TCT | 334 |
| Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser | |
| 100 105 110 | |
| GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG TTC GCT | 382 |
| Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala | |
| 115 120 125 | |
| CAG GGG TGG GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG GAC CAG | 430 |
| Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln | |
| 130 135 140 | |
| AGG CCC TAC TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT GTA CCC | 478 |
| Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro | |
| 145 150 155 | |
| GCG TCT CAG GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC CCT GTT | 526 |
| Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val | |
| 160 165 170 175 | |
| GTG GTG GGG ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC TGG GGG | 574 |
| Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly | |
| 180 185 190 | |
| GCG AAC GAC TCG GAT GTG CTG ATT CTC AAC AAC ACG CGG CCG CCG CGA | 622 |
| Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg | |
| 195 200 205 | |

| | |
|---|------|
| GGC AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys 210 215 220 | 670 |
| ACG TGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr 225 230 235 | 718 |
| TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC ACC TAC Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr 240 245 250 255 | 766 |
| GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG GTT CAT Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His 260 265 270 | 814 |
| TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC ACC ATC Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile 275 280 285 | 862 |
| TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC GAA GCC Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala 290 295 300 | 910 |
| GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC AGG GAT Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp 305 310 315 | 958 |
| AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GGT GAT CGA GGG Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Gly Asp Arg Gly 320 325 330 335 | 1006 |
| CAG ACA CCA TCA CCA CCA TCA CTA AT AG Gln Thr Pro Ser Pro Pro Ser Leu 340 | 1034 |

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 343 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

| |
|--|
| Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val 1 5 10 15 |
| Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val 20 25 30 |
| Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val 35 40 45 |
| Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe 50 55 60 |
| Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser 65 70 75 80 |

Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr
 85 90 95
 Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly
 100 105 110
 Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln
 115 120 125
 Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg
 130 135 140
 Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala
 145 150 155 160
 Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val
 165 170 175
 Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala
 180 185 190
 Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly
 195 200 205
 Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr
 210 215 220
 Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu
 225 230 235 240
 Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala
 245 250 255
 Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr
 260 265 270
 Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe
 275 280 285
 Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala
 290 295 300
 Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg
 305 310 315 320
 Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Gly Asp Arg Gly Gln
 325 330 335
 Thr Pro Ser Pro Pro Ser Leu
 340

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 945 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..942

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1..939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

| | |
|---|-----|
| ATG GTG GGG AAC TGG GCT AAG GTT TTG GTT GTG ATG CTA CTC TTT GCC | 48 |
| Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala | |
| 1 5 10 15 | |
| GGC GTC GAC GGG CAT ACC CGC GTG TCA GGA GGG GCA GCA GCC TCC GAT | 96 |
| Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp | |
| 20 25 30 | |
| ACC AGG GGC CTT GTG TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA ATC | 144 |
| Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile | |
| 35 40 45 | |
| CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC CTG | 192 |
| Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu | |
| 50 55 60 | |
| AAC TGC AAC GAC TCC CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC TAC | 240 |
| Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr | |
| 65 70 75 80 | |
| AAA CAC AAA TTC AAC TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC TGT | 288 |
| Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys | |
| 85 90 95 | |
| CGC TCC ATC GAC AAG TTC GCT CAG GGG TGG GGT CCC CTC ACT TAC ACT | 336 |
| Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr | |
| 100 105 110 | |
| GAG CCT AAC AGC TCG GAC CAG AGG CCC TAC TGC TGG CAC TAC GCG CCT | 384 |
| Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro | |
| 115 120 125 | |
| CGA CCG TGT GGT ATT GTA CCC GCG TCT CAG GTG TGC GGT CCA GTG TAT | 432 |
| Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr | |
| 130 135 140 | |
| TGC TTC ACC CCG AGC CCT GTT GTG GTG GGG ACG ACC GAT CGG TTT GGT | 480 |
| Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly | |
| 145 150 155 160 | |
| GTC CCC ACG TAT AAC TGG GGG GCG AAC GAC TCG GAT GTG CTG ATT CTC | 528 |
| Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu | |
| 165 170 175 | |
| AAC AAC ACG CGG CCG CCG CGA GGC AAC TGG TTC GGC TGT ACA TGG ATG | 576 |
| Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met | |
| 180 185 190 | |

| | |
|---|-----|
| AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC ATC | 624 |
| Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile | |
| 195 200 205 | |
| GGG GGG GCC GGC AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG | 672 |
| Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg | |
| 210 215 220 | |
| AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG | 720 |
| Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu | |
| 225 230 235 240 | |
| ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC CCC | 768 |
| Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro | |
| 245 250 255 | |
| TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG GGC | 816 |
| Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly | |
| 260 265 270 | |
| GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG CGT | 864 |
| Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg | |
| 275 280 285 | |
| TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG CTG | 912 |
| Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu | |
| 290 295 300 | |
| TCT ACA ACA GAG TGG CAG AGC TTA ATT AAT TAG | 945 |
| Ser Thr Thr Glu Trp Gln Ser Leu Ile Asn | |
| 305 310 | |

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

| | |
|---|--|
| Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala | |
| 1 5 10 15 | |
| Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp | |
| 20 25 30 | |
| Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile | |
| 35 40 45 | |
| Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu | |
| 50 55 60 | |
| Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr | |
| 65 70 75 80 | |
| Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys | |
| 85 90 95 | |

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Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr
      100                      105                      110

Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro
      115                      120                      125

Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr
      130                      135                      140

Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly
      145                      150                      155                      160

Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu
      165                      170                      175

Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met
      180                      185                      190

Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile
      195                      200                      205

Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg
      210                      215                      220

Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu
      225                      230                      235                      240

Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro
      245                      250                      255

Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly
      260                      265                      270

Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg
      275                      280                      285

Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu
      290                      295                      300

Ser Thr Thr Glu Trp Gln Ser Leu Ile Asn
      305                      310

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(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 961 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..958

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide

(B) LOCATION: 1..955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

| | |
|---|-----|
| ATG GTG GGG AAC TGG GCT AAG GTT TTG GTT GTG ATG CTA CTC TTT GCC | 48 |
| Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala | |
| 1 5 10 15 | |
| GGC GTC GAC GGG CAT ACC CGC GTG TCA GGA GGG GCA GCA GCC TCC GAT | 96 |
| Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ser Asp | |
| 20 25 30 | |
| ACC AGG GGC CTT GTG TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA ATC | 144 |
| Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile | |
| 35 40 45 | |
| CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC CTG | 192 |
| Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu | |
| 50 55 60 | |
| AAC TGC AAC GAC TCC CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC TAC | 240 |
| Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr | |
| 65 70 75 80 | |
| AAA CAC AAA TTC AAC TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC TGT | 288 |
| Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys | |
| 85 90 95 | |
| CGC TCC ATC GAC AAG TTC GCT CAG GGG TGG GGT CCC CTC ACT TAC ACT | 336 |
| Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr | |
| 100 105 110 | |
| GAG CCT AAC AGC TCG GAC CAG AGG CCC TAC TGC TGG CAC TAC GCG CCT | 384 |
| Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro | |
| 115 120 125 | |
| CGA CCG TGT GGT ATT GTA CCC GCG TCT CAG GTG TGC GGT CCA GTG TAT | 432 |
| Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr | |
| 130 135 140 | |
| TGC TTC ACC CCG AGC CCT GTT GTG GTG GGG ACG ACC GAT CGG TTT GGT | 480 |
| Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly | |
| 145 150 155 160 | |
| GTC CCC ACG TAT AAC TGG GGG GCG AAC GAC TCG GAT GTG CTG ATT CTC | 528 |
| Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu | |
| 165 170 175 | |
| AAC AAC ACG CGG CCG CCG CGA GGC AAC TGG TTC GGC TGT ACA TGG ATG | 576 |
| Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met | |
| 180 185 190 | |
| AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC ATC | 624 |
| Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile | |
| 195 200 205 | |
| GGG GGG GCC GGC AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG | 672 |
| Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg | |
| 210 215 220 | |
| AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG | 720 |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Lys | His | Pro | Glu | Ala | Thr | Tyr | Ala | Arg | Cys | Gly | Ser | Gly | Pro | Trp | Leu | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | |
| ACA | CCT | AGG | TGT | ATG | GTT | CAT | TAC | CCA | TAT | AGG | CTC | TGG | CAC | TAC | CCC | 768 | |
| Thr | Pro | Arg | Cys | Met | Val | His | Tyr | Pro | Tyr | Arg | Leu | Trp | His | Tyr | Pro | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | |
| TGC | ACT | GTC | AAC | TTC | ACC | ATC | TTC | AAG | GTT | AGG | ATG | TAC | GTG | GGG | GGC | 816 | |
| Cys | Thr | Val | Asn | Phe | Thr | Ile | Phe | Lys | Val | Arg | Met | Tyr | Val | Gly | Gly | | |
| | | | | 260 | | | | | 265 | | | | | 270 | | | |
| GTG | GAG | CAC | AGG | TTC | GAA | GCC | GCA | TGC | AAT | TGG | ACT | CGA | GGA | GAG | CGT | 864 | |
| Val | Glu | His | Arg | Phe | Glu | Ala | Ala | Cys | Asn | Trp | Thr | Arg | Gly | Glu | Arg | | |
| | | | | 275 | | | 280 | | | | | | 285 | | | | |
| TGT | GAC | TTG | GAG | GAC | AGG | GAT | AGA | TCA | GAG | CTT | AGC | CCG | CTG | CTG | CTG | 912 | |
| Cys | Asp | Leu | Glu | Asp | Arg | Asp | Arg | Ser | Glu | Leu | Ser | Pro | Leu | Leu | Leu | | |
| | 290 | | | | | 295 | | | | | 300 | | | | | | |
| TCT | ACA | ACA | GGT | GAT | CGA | GGG | CAG | ACA | CCA | TCA | CCA | CCA | TCA | CTA | A | 958 | |
| Ser | Thr | Thr | Gly | Asp | Arg | Gly | Gln | Thr | Pro | Ser | Pro | Pro | Ser | Leu | | | |
| 305 | | | | | 310 | | | | | 315 | | | | | | | |
| TAG | | | | | | | | | | | | | | | | 961 | |

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 319 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Val | Gly | Asn | Trp | Ala | Lys | Val | Leu | Val | Val | Met | Leu | Leu | Phe | Ala | | |
| 1 | | | | | 5 | | | | 10 | | | | | 15 | | | |
| Gly | Val | Asp | Gly | His | Thr | Arg | Val | Ser | Gly | Gly | Ala | Ala | Ala | Ser | Asp | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | |
| Thr | Arg | Gly | Leu | Val | Ser | Leu | Phe | Ser | Pro | Gly | Ser | Ala | Gln | Lys | Ile | | |
| | | 35 | | | | 40 | | | | | | 45 | | | | | |
| Gln | Leu | Val | Asn | Thr | Asn | Gly | Ser | Trp | His | Ile | Asn | Arg | Thr | Ala | Leu | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | |
| Asn | Cys | Asn | Asp | Ser | Leu | Gln | Thr | Gly | Phe | Phe | Ala | Ala | Leu | Phe | Tyr | | |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | | | |
| Lys | His | Lys | Phe | Asn | Ser | Ser | Gly | Cys | Pro | Glu | Arg | Leu | Ala | Ser | Cys | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | | |
| Arg | Ser | Ile | Asp | Lys | Phe | Ala | Gln | Gly | Trp | Gly | Pro | Leu | Thr | Tyr | Thr | | |
| | | 100 | | | | | | 105 | | | | | 110 | | | | |
| Glu | Pro | Asn | Ser | Ser | Asp | Gln | Arg | Pro | Tyr | Cys | Trp | His | Tyr | Ala | Pro | | |
| | | 115 | | | | | 120 | | | | | | 125 | | | | |
| Arg | Pro | Cys | Gly | Ile | Val | Pro | Ala | Ser | Gln | Val | Cys | Gly | Pro | Val | Tyr | | |

| | | | | |
|---|-----|-----|-----|-----|
| 130 | | 135 | | 140 |
| Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly | | | | |
| 145 | | 150 | | 155 |
| Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu | | | | |
| | 165 | | 170 | 175 |
| Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met | | | | |
| | 180 | | 185 | 190 |
| Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile | | | | |
| | 195 | | 200 | 205 |
| Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg | | | | |
| | 210 | | 215 | 220 |
| Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu | | | | |
| 225 | | 230 | | 235 |
| Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro | | | | |
| | 245 | | 250 | 255 |
| Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly | | | | |
| | 260 | | 265 | 270 |
| Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg | | | | |
| | 275 | | 280 | 285 |
| Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu | | | | |
| 290 | | 295 | | 300 |
| Ser Thr Thr Gly Asp Arg Gly Gln Thr Pro Ser Pro Pro Ser Leu | | | | |
| 305 | | 310 | | 315 |

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1392

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG GGC CTC GCC TAC TAT

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ala | Gly | Ala | His | Trp | Gly | Val | Leu | Ala | Gly | Leu | Ala | Tyr | Tyr | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| TCC | ATG | GTG | GGG | AAC | TGG | GCT | AAG | GTT | TTG | GTT | GTG | ATG | CTA | CTC | TTT | 96 |
| Ser | Met | Val | Gly | Asn | Trp | Ala | Lys | Val | Leu | Val | Val | Met | Leu | Leu | Phe | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| GCC | GGC | GTC | GAC | GGG | CAT | ACC | CGC | GTG | TCA | GGA | GGG | GCA | GCA | GCC | TCC | 144 |
| Ala | Gly | Val | Asp | Gly | His | Thr | Arg | Val | Ser | Gly | Gly | Ala | Ala | Ala | Ser | |
| | | | 35 | | | | 40 | | | | | 45 | | | | |
| GAT | ACC | AGG | GGC | CTT | GTG | TCC | CTC | TTT | AGC | CCC | GGG | TCG | GCT | CAG | AAA | 192 |
| Asp | Thr | Arg | Gly | Leu | Val | Ser | Leu | Phe | Ser | Pro | Gly | Ser | Ala | Gln | Lys | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| ATC | CAG | CTC | GTA | AAC | ACC | AAC | GGC | AGT | TGG | CAC | ATC | AAC | AGG | ACT | GCC | 240 |
| Ile | Gln | Leu | Val | Asn | Thr | Asn | Gly | Ser | Trp | His | Ile | Asn | Arg | Thr | Ala | |
| | 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| CTG | AAC | TGC | AAC | GAC | TCC | CTC | CAA | ACA | GGG | TTC | TTT | GCC | GCA | CTA | TTC | 288 |
| Leu | Asn | Cys | Asn | Asp | Ser | Leu | Gln | Thr | Gly | Phe | Phe | Ala | Ala | Leu | Phe | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| TAC | AAA | CAC | AAA | TTC | AAC | TCG | TCT | GGA | TGC | CCA | GAG | CGC | TTG | GCC | AGC | 336 |
| Tyr | Lys | His | Lys | Phe | Asn | Ser | Ser | Gly | Cys | Pro | Glu | Arg | Leu | Ala | Ser | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| TGT | CGC | TCC | ATC | GAC | AAG | TTC | GCT | CAG | GGG | TGG | GGT | CCC | CTC | ACT | TAC | 384 |
| Cys | Arg | Ser | Ile | Asp | Lys | Phe | Ala | Gln | Gly | Trp | Gly | Pro | Leu | Thr | Tyr | |
| | | | 115 | | | | 120 | | | | | 125 | | | | |
| ACT | GAG | CCT | AAC | AGC | TCG | GAC | CAG | AGG | CCC | TAC | TGC | TGG | CAC | TAC | GCG | 432 |
| Thr | Glu | Pro | Asn | Ser | Ser | Asp | Gln | Arg | Pro | Tyr | Cys | Trp | His | Tyr | Ala | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| CCT | CGA | CCG | TGT | GGT | ATT | GTA | CCC | GCG | TCT | CAG | GTG | TGC | GGT | CCA | GTG | 480 |
| Pro | Arg | Pro | Cys | Gly | Ile | Val | Pro | Ala | Ser | Gln | Val | Cys | Gly | Pro | Val | |
| | 145 | | | | 150 | | | | | 155 | | | | | 160 | |
| TAT | TGC | TTC | ACC | CCG | AGC | CCT | GTT | GTG | GTG | GGG | ACG | ACC | GAT | CGG | TTT | 528 |
| Tyr | Cys | Phe | Thr | Pro | Ser | Pro | Val | Val | Val | Gly | Thr | Thr | Asp | Arg | Phe | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| GGT | GTC | CCC | ACG | TAT | AAC | TGG | GGG | GCG | AAC | GAC | TCG | GAT | GTG | CTG | ATT | 576 |
| Gly | Val | Pro | Thr | Tyr | Asn | Trp | Gly | Ala | Asn | Asp | Ser | Asp | Val | Leu | Ile | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| CTC | AAC | AAC | ACG | CGG | CCG | CCG | CGA | GGC | AAC | TGG | TTC | GGC | TGT | ACA | TGG | 624 |
| Leu | Asn | Asn | Thr | Arg | Pro | Pro | Arg | Gly | Asn | Trp | Phe | Gly | Cys | Thr | Trp | |
| | | | 195 | | | | 200 | | | | | 205 | | | | |
| ATG | AAT | GGC | ACT | GGG | TTC | ACC | AAG | ACG | TGT | GGG | GGC | CCC | CCG | TGC | AAC | 672 |
| Met | Asn | Gly | Thr | Gly | Phe | Thr | Lys | Thr | Cys | Gly | Gly | Pro | Pro | Cys | Asn | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| ATC | GGG | GGG | GCC | GGC | AAC | AAC | ACC | TTG | ACC | TGC | CCC | ACT | GAC | TGT | TTT | 720 |
| Ile | Gly | Gly | Ala | Gly | Asn | Asn | Thr | Leu | Thr | Cys | Pro | Thr | Asp | Cys | Phe | |
| | 225 | | | | 230 | | | | | 235 | | | | | 240 | |
| CGG | AAG | CAC | CCC | GAG | GCC | ACC | TAC | GCC | AGA | TGC | GGT | TCT | GGG | CCC | TGG | 768 |
| Arg | Lys | His | Pro | Glu | Ala | Thr | Tyr | Ala | Arg | Cys | Gly | Ser | Gly | Pro | Trp | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |

| | |
|--|------|
| CTG ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC | 816 |
| Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr | |
| 260 265 270 | |
| CCC TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG | 864 |
| Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly | |
| 275 280 285 | |
| GGC GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG | 912 |
| Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu | |
| 290 295 300 | |
| CGT TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG | 960 |
| Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu | |
| 305 310 315 320 | |
| CTG TCT ACA ACA GAG TGG CAG ATA CTG CCC TGT TCC TTC ACC ACC CTG | 1008 |
| Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu | |
| 325 330 335 | |
| CCG GCC CTA TCC ACC GGC CTG ATC CAC CTC CAT CAG AAC ATC GTG GAC | 1056 |
| Pro Ala Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp | |
| 340 345 350 | |
| GTG CAA TAC CTG TAC GGT GTA GGG TCG GCG GTT GTC TCC CTT GTC ATC | 1104 |
| Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile | |
| 355 360 365 | |
| AAA TGG GAG TAT GTC CTG TTG CTC TTC CTT CTC CTG GCA GAC GCG CGC | 1152 |
| Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg | |
| 370 375 380 | |
| ATC TGC GCC TGC TTA TGG ATG ATG CTG CTG ATA GCT CAA GCT GAG GCC | 1200 |
| Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala | |
| 385 390 395 400 | |
| GCC TTA GAG AAC CTG GTG GTC CTC AAT GCG GCG GCC GTG GCC GGG GCG | 1248 |
| Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala Ala Val Ala Gly Ala | |
| 405 410 415 | |
| CAT GGC ACT CTT TCC TTC CTT GTG TTC TTC TGT GCT GCC TGG TAC ATC | 1296 |
| His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile | |
| 420 425 430 | |
| AAG GGC AGG CTG GTC CCT GGT GCG GCA TAC GCC TTC TAT GGC GTG TGG | 1344 |
| Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp | |
| 435 440 445 | |
| CCG CTG CTC CTG CTT CTG CTG GCC TTA CCA CCA CGA GCT TAT GCC TAGTAA | 1395 |
| Pro Leu Leu Leu Leu Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala | |
| 450 455 460 | |

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 463 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

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Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr
 1              5              10              15

Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe
          20          25          30
Ala Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser
          35          40          45

Asp Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys
 50          55          60

Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala
 65          70          75          80

Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe
          85          90          95

Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser
          100          105          110

Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr
          115          120          125

Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala
          130          135          140

Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val
          145          150          155          160

Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe
          165          170          175

Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile
          180          185          190

Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp
          195          200          205

Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn
          210          215          220

Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe
          225          230          235          240

Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp
          245          250          255

Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr
          260          265          270

Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly
          275          280          285

Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu
          290          295          300

Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu
          305          310          315          320

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Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu
 325 330 335
 Pro Ala Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp
 340 345 350
 Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile
 355 360 365
 Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg
 370 375 380
 Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala
 385 390 395 400
 Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala Val Ala Gly Ala
 405 410 415
 His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile
 420 425 430
 Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp
 435 440 445
 Pro Leu Leu Leu Leu Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala
 450 455 460

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2079

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..2076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

AAT TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC
 Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu
 1 5 10 15
 GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG
 Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg
 20 25 30

48

96

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GCC | CTG | GCG | CAT | GGC | GTC | CGG | GTT | CTG | GAG | GAC | GGC | GTG | AAC | TAT | GCA | 144 |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| ACA | GGG | AAT | TTG | CCC | GGT | TGC | TCT | TTC | TCT | ATC | TTC | CTC | TTG | GCT | TTG | 192 |
| Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| CTG | TCC | TGT | CTG | ACC | GTT | CCA | GCT | TCC | GCT | TAT | GAA | GTG | CGC | AAC | GTG | 240 |
| Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| TCC | GGG | ATG | TAC | CAT | GTC | ACG | AAC | GAC | TGC | TCC | AAC | TCA | AGC | ATT | GTG | 288 |
| Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| TAT | GAG | GCA | GCG | GAC | ATG | ATC | ATG | CAC | ACC | CCC | GGG | TGC | GTG | CCC | TGC | 336 |
| Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr | Pro | Gly | Cys | Val | Pro | Cys | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| GTT | CGG | GAG | AAC | AAC | TCT | TCC | CGC | TGC | TGG | GTA | GCG | CTC | ACC | CCC | ACG | 384 |
| Val | Arg | Glu | Asn | Asn | Ser | Ser | Arg | Cys | Trp | Val | Ala | Leu | Thr | Pro | Thr | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| CTC | GCA | GCT | AGG | AAC | GCC | AGC | GTC | CCC | ACC | ACG | ACA | ATA | CGA | CGC | CAC | 432 |
| Leu | Ala | Ala | Arg | Asn | Ala | Ser | Val | Pro | Thr | Thr | Thr | Ile | Arg | Arg | His | |
| | | 130 | | | | | 135 | | | | | 140 | | | | |
| GTC | GAT | TTG | CTC | GTT | GGG | GCG | GCT | GCT | TTC | TGT | TCC | GCT | ATG | TAC | GTG | 480 |
| Val | Asp | Leu | Leu | Val | Gly | Ala | Ala | Ala | Phe | Cys | Ser | Ala | Met | Tyr | Val | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| GGG | GAC | CTC | TGC | GGA | TCT | GTC | TTC | CTC | GTC | TCC | CAG | CTG | TTC | ACC | ATC | 528 |
| Gly | Asp | Leu | Cys | Gly | Ser | Val | Phe | Leu | Val | Ser | Gln | Leu | Phe | Thr | Ile | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| TCG | CCT | CGC | CGG | CAT | GAG | ACG | GTG | CAG | GAC | TGC | AAT | TGC | TCA | ATC | TAT | 576 |
| Ser | Pro | Arg | Arg | His | Glu | Thr | Val | Gln | Asp | Cys | Asn | Cys | Ser | Ile | Tyr | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| CCC | GGC | CAC | ATA | ACG | GGT | CAC | CGT | ATG | GCT | TGG | GAT | ATG | ATG | ATG | AAC | 624 |
| Pro | Gly | His | Ile | Thr | Gly | His | Arg | Met | Ala | Trp | Asp | Met | Met | Met | Asn | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| TGG | TCG | CCT | ACA | ACG | GCC | CTG | GTG | GTA | TCG | CAG | CTG | CTC | CGG | ATC | CCA | 672 |
| Trp | Ser | Pro | Thr | Thr | Ala | Leu | Val | Val | Ser | Gln | Leu | Leu | Arg | Ile | Pro | |
| | 210 | | | | | 215 | | | | | | 220 | | | | |
| CAA | GCT | GTC | GTG | GAC | ATG | GTG | GCG | GGG | GCC | CAT | TGG | GGA | GTC | CTG | GCG | 720 |
| Gln | Ala | Val | Val | Asp | Met | Val | Ala | Gly | Ala | His | Trp | Gly | Val | Leu | Ala | |
| 225 | | | | | | 230 | | | | 235 | | | | | 240 | |
| GGC | CTC | GCC | TAC | TAT | TCC | ATG | GTG | GGG | AAC | TGG | GCT | AAG | GTT | TTG | GTT | 768 |
| Gly | Leu | Ala | Tyr | Tyr | Ser | Met | Val | Gly | Asn | Trp | Ala | Lys | Val | Leu | Val | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| GTG | ATG | CTA | CTC | TTT | GCC | GGC | GTC | GAC | GGG | CAT | ACC | CGC | GTG | TCA | GGA | 816 |
| Val | Met | Leu | Leu | Phe | Ala | Gly | Val | Asp | Gly | His | Thr | Arg | Val | Ser | Gly | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| GGG | GCA | GCA | GCC | TCC | GAT | ACC | AGG | GGC | CTT | GTG | TCC | CTC | TTT | AGC | CCC | 864 |
| Gly | Ala | Ala | Ala | Ser | Asp | Thr | Arg | Gly | Leu | Val | Ser | Leu | Phe | Ser | Pro | |

| 275 | | | | | 280 | | | | | 285 | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| GGG Gly | TCG Ser | GCT Ala | CAG Gln | AAA Lys | ATC Ile | CAG Gln | CTC Leu | GTA Val | AAC Asn | ACC Thr | AAC Asn | GGC Gly | AGT Ser | TGG Trp | CAC His | 912 |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| ATC Ile | AAC Asn | AGG Arg | ACT Thr | GCC Ala | CTG Leu | AAC Asn | TGC Cys | AAC Asn | GAC Asp | TCC Ser | CTC Leu | CAA Gln | ACA Thr | GGG Gly | TTC Phe | 960 |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| TTT Phe | GCC Ala | GCA Ala | CTA Leu | TTC Phe | TAC Tyr | AAA Lys | CAC His | AAA Lys | TTC Phe | AAC Asn | TCG Ser | TCT Ser | GGA Gly | TGC Cys | CCA Pro | 1008 |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| GAG Glu | CGC Arg | TTG Leu | GCC Ala | AGC Ser | TGT Cys | CGC Arg | TCC Ser | ATC Ile | GAC Asp | AAG Lys | TTC Phe | GCT Ala | CAG Gln | GGG Gly | TGG Trp | 1056 |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| GGT Gly | CCC Pro | CTC Leu | ACT Thr | TAC Tyr | ACT Thr | GAG Glu | CCT Pro | AAC Asn | AGC Ser | TCG Ser | GAC Asp | CAG Gln | AGG Arg | CCC Pro | TAC Tyr | 1104 |
| | | 355 | | | | | 360 | | | | | 365 | | | | |
| TGC Cys | TGG Trp | CAC His | TAC Tyr | GCG Ala | CCT Pro | CGA Arg | CCG Pro | TGT Cys | GGT Gly | ATT Ile | GTA Val | CCC Pro | GCG Ala | TCT Ser | CAG Gln | 1152 |
| | 370 | | | | | 375 | | | | | 380 | | | | | |
| GTG Val | TGC Cys | GGT Gly | CCA Pro | GTG Val | TAT Tyr | TGC Cys | TTC Phe | ACC Thr | CCG Pro | AGC Ser | CCT Pro | GTT Val | GTG Val | GTG Val | GGG Gly | 1200 |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| ACG Thr | ACC Thr | GAT Asp | CGG Arg | TTT Phe | GGT Gly | GTC Val | CCC Pro | ACG Thr | TAT Tyr | AAC Asn | TGG Trp | GGG Gly | GCG Ala | AAC Asn | GAC Asp | 1248 |
| | | | | 405 | | | | | 410 | | | | | 415 | | |
| TCG Ser | GAT Asp | GTG Val | CTG Leu | ATT Ile | CTC Leu | AAC Asn | AAC Asn | ACG Thr | CGG Arg | CCG Pro | CCG Pro | CGA Arg | GGC Gly | AAC Asn | TGG Trp | 1296 |
| | | | 420 | | | | | 425 | | | | | 430 | | | |
| TTC Phe | GGC Gly | TGT Cys | ACA Thr | TGG Trp | ATG Met | AAT Asn | GGC Gly | ACT Thr | GGG Gly | TTC Phe | ACC Thr | AAG Lys | ACG Thr | TGT Cys | GGG Gly | 1344 |
| | | 435 | | | | | 440 | | | | | 445 | | | | |
| GGC Gly | CCC Pro | CCG Pro | TGC Cys | AAC Asn | ATC Ile | GGG Gly | GGG Gly | GCC Ala | GGC Gly | AAC Asn | AAC Asn | ACC Thr | TTG Leu | ACC Thr | TGC Cys | 1392 |
| | 450 | | | | | 455 | | | | | 460 | | | | | |
| CCC Pro | ACT Thr | GAC Asp | TGT Cys | TTT Phe | CGG Arg | AAG Lys | CAC His | CCC Pro | GAG Glu | GCC Ala | ACC Thr | TAC Tyr | GCC Ala | AGA Arg | TGC Cys | 1440 |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 | |
| GGT Gly | TCT Ser | GGG Gly | CCC Pro | TGG Trp | CTG Leu | ACA Thr | CCT Pro | AGG Arg | TGT Cys | ATG Met | GTT Val | CAT His | TAC Tyr | CCA Pro | TAT Tyr | 1488 |
| | | | | 485 | | | | 490 | | | | | | 495 | | |
| AGG Arg | CTC Leu | TGG Trp | CAC His | TAC Tyr | CCC Pro | TGC Cys | ACT Thr | GTC Val | AAC Asn | TTC Phe | ACC Thr | ATC Ile | TTT Phe | AAG Lys | GTT | |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|--------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Trp | Thr | Arg | Gly | Glu | Arg | Cys | Asp | Leu | Glu | Asp | Arg | Asp | Arg | Ser | Glu | | |
| 530 | | | | | | 535 | | | | | 540 | | | | | | |
| CTT | AGC | CCG | CTG | CTG | CTG | TCT | ACA | ACA | GAG | TGG | CAG | ATA | CTG | CCC | TGT | 1680 | |
| Leu | Ser | Pro | Leu | Leu | Leu | Ser | Thr | Thr | Glu | Trp | Gln | Ile | Leu | Pro | Cys | | |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 | | |
| TCC | TTC | ACC | ACC | CTG | CCG | GCC | CTA | TCC | ACC | GGC | CTG | ATC | CAC | CTC | CAT | 1728 | |
| Ser | Phe | Thr | Thr | Leu | Pro | Ala | Leu | Ser | Thr | Gly | Leu | Ile | His | Leu | His | | |
| | | | | 565 | | | | | 570 | | | | | 575 | | | |
| CAG | AAC | ATC | GTG | GAC | GTG | CAA | TAC | CTG | TAC | GGT | GTA | GGG | TCG | GCG | GTT | 1776 | |
| Gln | Asn | Ile | Val | Asp | Val | Gln | Tyr | Leu | Tyr | Gly | Val | Gly | Ser | Ala | Val | | |
| | | | 580 | | | | | 585 | | | | | 590 | | | | |
| GTC | TCC | CTT | GTC | ATC | AAA | TGG | GAG | TAT | GTC | CTG | TTG | CTC | TTC | CTT | CTC | 1824 | |
| Val | Ser | Leu | Val | Ile | Lys | Trp | Glu | Tyr | Val | Leu | Leu | Leu | Phe | Leu | Leu | | |
| | | 595 | | | | 600 | | | | | | 605 | | | | | |
| CTG | GCA | GAC | GCG | CGC | ATC | TGC | GCC | TGC | TTA | TGG | ATG | ATG | CTG | CTG | ATA | 1872 | |
| Leu | Ala | Asp | Ala | Arg | Ile | Cys | Ala | Cys | Leu | Trp | Met | Met | Leu | Leu | Ile | | |
| | 610 | | | | | 615 | | | | | 620 | | | | | | |
| GCT | CAA | GCT | GAG | GCC | GCC | TTA | GAG | AAC | CTG | GTG | GTC | CTC | AAT | GCG | GCG | 1920 | |
| Ala | Gln | Ala | Glu | Ala | Ala | Leu | Glu | Asn | Leu | Val | Val | Leu | Asn | Ala | Ala | | |
| 625 | | | | | 630 | | | | | 635 | | | | | 640 | | |
| GCC | GTG | GCC | GGG | GCG | CAT | GGC | ACT | CTT | TCC | TTC | CTT | GTG | TTC | TTC | TGT | 1968 | |
| Ala | Val | Ala | Gly | Ala | His | Gly | Thr | Leu | Ser | Phe | Leu | Val | Phe | Phe | Cys | | |
| | | | | 645 | | | | | 650 | | | | | 655 | | | |
| GCT | GCC | TGG | TAC | ATC | AAG | GGC | AGG | CTG | GTC | CCT | GGT | GCG | GCA | TAC | GCC | 2016 | |
| Ala | Ala | Trp | Tyr | Ile | Lys | Gly | Arg | Leu | Val | Pro | Gly | Ala | Ala | Tyr | Ala | | |
| | | | 660 | | | | | 665 | | | | | 670 | | | | |
| TTC | TAT | GGC | GTG | TGG | CCG | CTG | CTC | CTG | CTT | CTG | CTG | GCC | TTA | CCA | CCA | 2064 | |
| Phe | Tyr | Gly | Val | Trp | Pro | Leu | Leu | Leu | Leu | Leu | Leu | Ala | Leu | Pro | Pro | | |
| | | 675 | | | | 680 | | | | | | 685 | | | | | |
| CGA | GCT | TAT | GCC | TAGTAA | | | | | | | | | | | | 2082 | |
| Arg | Ala | Tyr | Ala | | | | | | | | | | | | | | |
| | | | 690 | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Asn | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | |
| Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu | Gly | Gly | Ala | Ala | Arg | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala | | |

35

40

45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu
 50 55 60
 Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val
 65 70 75 80
 Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val
 85 90 95
 Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
 100 105 110
 Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
 115 120 125
 Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His
 130 135 140
 Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val
 145 150 155 160
 Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile
 165 170 175
 Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr
 180 185 190
 Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn
 195 200 205
 Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 210 215 220
 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala
 225 230 235 240
 Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Val
 245 250 255
 Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val Ser Gly
 260 265 270
 Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe Ser Pro
 275 280 285
 Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His
 290 295 300
 Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe
 305 310 315 320
 Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro
 325 330 335
 Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp
 340 345 350
 Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr
 355 360 365
 Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln

| | | |
|---|---------|---------|
| 370 | 375 | 380 |
| Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly | | |
| 385 | 390 | 395 400 |
| Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp | | |
| | 405 410 | 415 |
| Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp | | |
| | 420 425 | 430 |
| Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly | | |
| | 435 440 | 445 |
| Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys | | |
| | 450 455 | 460 |
| Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys | | |
| | 465 470 | 475 480 |
| Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr | | |
| | 485 490 | 495 |
| Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val | | |
| | 500 505 | 510 |
| Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn | | |
| | 515 520 | 525 |
| Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu | | |
| | 530 535 | 540 |
| Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys | | |
| | 545 550 | 555 560 |
| Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly Leu Ile His Leu His | | |
| | 565 570 | 575 |
| Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val | | |
| | 580 585 | 590 |
| Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu | | |
| | 595 600 | 605 |
| Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile | | |
| | 610 615 | 620 |
| Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala | | |
| | 625 630 | 635 640 |
| Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys | | |
| | 645 650 | 655 |
| Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala | | |
| | 660 665 | 670 |
| Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu Leu Ala Leu Pro Pro | | |
| | 675 680 | 685 |
| Arg Ala Tyr Ala | | |
| 690 | | |

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2433 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..2430

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..2427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

| | |
|---|-----|
| ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC | 48 |
| Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn | |
| 1 5 10 15 | |
| CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT GGT | 96 |
| Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly | |
| 20 25 30 | |
| GGA GTT TAC CTG TTG CCG CGC AGG GGC CCC AGG TTG GGT GTG CGC GCG | 144 |
| Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala | |
| 35 40 45 | |
| ACT AGG AAG ACT TCC GAG CGG TCG CAA CCT CGT GGG AGG CGA CAA CCT | 192 |
| Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro | |
| 50 55 60 | |
| ATC CCC AAG GCT CGC CGA CCC GAG GGT AGG GCC TGG GCT CAG CCC GGG | 240 |
| Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly | |
| 65 70 75 80 | |
| TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC ATG GGG TGG GCA GGA TGG | 288 |
| Tyr Pro Trp Pro Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp | |
| 85 90 95 | |
| CTC CTG TCA CCC CGC GGC TCT CGG CCT AGT TGG GGC CCT ACA GAC CCC | 336 |
| Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro | |
| 100 105 110 | |
| CGG CGT AGG TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC | 384 |
| Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys | |
| 115 120 125 | |
| GGC TTC GCC GAC CTC GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA | 432 |
| Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu | |
| 130 135 140 | |
| GGG GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC | 480 |

| | | | | | | | | | | | | | | | | |
|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|------|
| Gly 145 | Gly | Ala | Ala | Arg | Ala 150 | Leu | Ala | His | Gly | Val 155 | Arg | Val | Leu | Glu | Asp 160 | |
| GGC Gly | GTG Val | AAC Asn | TAT Tyr | GCA Ala 165 | ACA Thr | GGG Gly | AAT Asn | TTG Leu | CCC Pro 170 | GGT Gly | TGC Cys | TCT Ser | TTC Phe | TCT Ser | ATC Ile 175 | 528 |
| TTC Phe | CTC Leu | TTG Leu | GCT Ala 180 | TTG Leu | CTG Leu | TCC Ser | TGT Cys | CTG Leu 185 | ACC Thr | GTT Val | CCA Pro | GCT Ala | TCC Ser | GCT Ala | TAT Tyr | 576 |
| GAA Glu | GTG Val | CGC Arg | AAC Asn 195 | GTG Val | TCC Ser | GGG Gly | ATG Met 200 | TAC Tyr | CAT His | GTC Val | ACG Thr | AAC Asn 205 | GAC Asp | TGC Cys | TCC Ser | 624 |
| AAC Asn 210 | TCA Ser | AGC Ser | ATT Ile | GTG Val | TAT Tyr | GAG Glu 215 | GCA Ala | GCG Ala | GAC Asp | ATG Met | ATC Ile | ATG Met | CAC His | ACC Thr | CCC Pro | 672 |
| GGG Gly 225 | TGC Cys | GTG Val | CCC Pro | TGC Cys | GTT Val 230 | CGG Arg | GAG Glu | AAC Asn | AAC Asn | TCT Ser 235 | TCC Ser | CGC Arg | TGC Cys | TGG Trp | GTA Val 240 | 720 |
| GCG Ala | CTC Leu | ACC Thr | CCC Pro | ACG Thr 245 | CTC Leu | GCA Ala | GCT Ala | AGG Arg | AAC Asn 250 | GCC Ala | AGC Ser | GTC Val | CCC Pro | ACC Thr | ACG Thr | 768 |
| ACA Thr | ATA Ile | CGA Arg | CGC Arg 260 | CAC His | GTC Val | GAT Asp | TTG Leu | CTC Leu 265 | GTT Val | GGG Gly | GCG Ala | GCT Ala | GCT Ala | TTC Phe | TGT Cys | 816 |
| TCC Ser | GCT Ala | ATG Met 275 | TAC Tyr | GTG Val | GGG Gly | GAC Asp | CTC Leu 280 | TGC Cys | GGA Gly | TCT Ser | GTC Val | TTC Phe | CTC Leu | GTC Val | TCC Ser | 864 |
| CAG Gln 290 | CTG Leu | TTC Phe | ACC Thr | ATC Ile | TCG Ser | CCT Pro 295 | CGC Arg | CGG Arg | CAT His | GAG Glu | ACG Thr | GTG Val | CAG Gln | GAC Asp | TGC Cys | 912 |
| AAT Asn 305 | TGC Cys | TCA Ser | ATC Ile | TAT Tyr | CCC Pro 310 | GGC Gly | CAC His | ATA Ile | ACG Thr | GGT Gly 315 | CAC His | CGT Arg | ATG Met | GCT Ala | TGG Trp 320 | 960 |
| GAT Asp | ATG Met | ATG Met | ATG Met | AAC Asn 325 | TGG Trp | TCG Ser | CCT Pro | ACA Thr | ACG Thr | GCC Ala 330 | CTG Leu | GTG Val | GTA Val | TCG Ser | CAG Gln | 1008 |
| CTG Leu | CTC Leu | CGG Arg | ATC Ile 340 | CCA Pro | CAA Gln | GCT Ala | GTC Val | GTG Val 345 | GAC Asp | ATG Met | GTG Val | GCG Ala | GGG Gly 350 | GCC Ala | CAT His | 1056 |
| TGG Trp | GGA Gly | GTC Val | CTG Leu | GCG Ala | GGC Gly | CTC Leu | GCC Ala | TAC Tyr 360 | TAT Tyr | TCC Ser | ATG Met | GTG Val | GGG Gly | AAC Asn | TGG Trp | 1104 |
| GCT Ala 370 | AAG Lys | GTT Val | TTG Leu | GTT Val | GTG Val | ATG Met 375 | CTA Leu | CTC Leu | TTT Phe | GCC Ala | GGC Gly 380 | GTC Val | GAC Asp | GGG Gly | CAT His | 1152 |
| ACC Thr 385 | CGC Arg | GTG Val | TCA Ser | GGA Gly | GGG Gly 390 | GCA Ala | GCA Ala | GCC Ala | TCC Ser | GAT Asp 395 | ACC Thr | AGG Arg | GGC Gly | CTT Leu | GTG Val 400 | 1200 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| TCC | CTC | TTT | AGC | CCC | GGG | TCG | GCT | CAG | AAA | ATC | CAG | CTC | GTA | AAC | ACC | 1248 |
| Ser | Leu | Phe | Ser | Pro | Gly | Ser | Ala | Gln | Lys | Ile | Gln | Leu | Val | Asn | Thr | |
| | | | | 405 | | | | | 410 | | | | | 415 | | |
| AAC | GGC | AGT | TGG | CAC | ATC | AAC | AGG | ACT | GCC | CTG | AAC | TGC | AAC | GAC | TCC | 1296 |
| Asn | Gly | Ser | Trp | His | Ile | Asn | Arg | Thr | Ala | Leu | Asn | Cys | Asn | Asp | Ser | |
| | | | 420 | | | | | 425 | | | | | 430 | | | |
| CTC | CAA | ACA | GGG | TTC | TTT | GCC | GCA | CTA | TTC | TAC | AAA | CAC | AAA | TTC | AAC | 1344 |
| Leu | Gln | Thr | Gly | Phe | Phe | Ala | Ala | Leu | Phe | Tyr | Lys | His | Lys | Phe | Asn | |
| | | 435 | | | | | 440 | | | | | 445 | | | | |
| TCG | TCT | GGA | TGC | CCA | GAG | CGC | TTG | GCC | AGC | TGT | CGC | TCC | ATC | GAC | AAG | 1392 |
| Ser | Ser | Gly | Cys | Pro | Glu | Arg | Leu | Ala | Ser | Cys | Arg | Ser | Ile | Asp | Lys | |
| | 450 | | | | | 455 | | | | | 460 | | | | | |
| TTC | GCT | CAG | GGG | TGG | GGT | CCC | CTC | ACT | TAC | ACT | GAG | CCT | AAC | AGC | TCG | 1440 |
| Phe | Ala | Gln | Gly | Trp | Gly | Pro | Leu | Thr | Tyr | Thr | Glu | Pro | Asn | Ser | Ser | |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 | |
| GAC | CAG | AGG | CCC | TAC | TGC | TGG | CAC | TAC | GCG | CCT | CGA | CCG | TGT | GGT | ATT | 1488 |
| Asp | Gln | Arg | Pro | Tyr | Cys | Trp | His | Tyr | Ala | Pro | Arg | Pro | Cys | Gly | Ile | |
| | | | | 485 | | | | | 490 | | | | | 495 | | |
| GTA | CCC | GCG | TCT | CAG | GTG | TGC | GGT | CCA | GTG | TAT | TGC | TTC | ACC | CCG | AGC | 1536 |
| Val | Pro | Ala | Ser | Gln | Val | Cys | Gly | Pro | Val | Tyr | Cys | Phe | Thr | Pro | Ser | |
| | | | 500 | | | | | 505 | | | | | 510 | | | |
| CCT | GTT | GTG | GTG | GGG | ACG | ACC | GAT | CGG | TTT | GGT | GTC | CCC | ACG | TAT | AAC | 1584 |
| Pro | Val | Val | Val | Gly | Thr | Thr | Asp | Arg | Phe | Gly | Val | Pro | Thr | Tyr | Asn | |
| | | 515 | | | | | 520 | | | | | 525 | | | | |
| TGG | GGG | GCG | AAC | GAC | TCG | GAT | GTG | CTG | ATT | CTC | AAC | AAC | ACG | CGG | CCG | 1632 |
| Trp | Gly | Ala | Asn | Asp | Ser | Asp | Val | Leu | Ile | Leu | Asn | Asn | Thr | Arg | Pro | |
| | 530 | | | | | 535 | | | | | 540 | | | | | |
| CCG | CGA | GGC | AAC | TGG | TTC | GGC | TGT | ACA | TGG | ATG | AAT | GGC | ACT | GGG | TTC | 1680 |
| Pro | Arg | Gly | Asn | Trp | Phe | Gly | Cys | Thr | Trp | Met | Asn | Gly | Thr | Gly | Phe | |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 | |
| ACC | AAG | ACG | TGT | GGG | GGC | CCC | CCG | TGC | AAC | ATC | GGG | GGG | GCC | GGC | AAC | 1728 |
| Thr | Lys | Thr | Cys | Gly | Gly | Pro | Pro | Cys | Asn | Ile | Gly | Gly | Ala | Gly | Asn | |
| | | | | 565 | | | | | 570 | | | | | 575 | | |
| AAC | ACC | TTG | ACC | TGC | CCC | ACT | GAC | TGT | TTT | CGG | AAG | CAC | CCC | GAG | GCC | 1776 |
| Asn | Thr | Leu | Thr | Cys | Pro | Thr | Asp | Cys | Phe | Arg | Lys | His | Pro | Glu | Ala | |
| | | | 580 | | | | | 585 | | | | | 590 | | | |
| ACC | TAC | GCC | AGA | TGC | GGT | TCT | GGG | CCC | TGG | CTG | ACA | CCT | AGG | TGT | ATG | 1824 |
| Thr | Tyr | Ala | Arg | Cys | Gly | Ser | Gly | Pro | Trp | Leu | Thr | Pro | Arg | Cys | Met | |
| | | 595 | | | | | 600 | | | | | 605 | | | | |
| GTT | CAT | TAC | CCA | TAT | AGG | CTC | TGG | CAC | TAC | CCC | TGC | ACT | GTC | AAC | TTC | 1872 |
| Val | His | Tyr | Pro | Tyr | Arg | Leu | Trp | His | Tyr | Pro | Cys | Thr | Val | Asn | Phe | |
| | 610 | | | | | 615 | | | | | 620 | | | | | |
| ACC | ATC | TTC | AAG | GTT | AGG | ATG | TAC | GTG | GGG | GGC | GTG | GAG | CAC | AGG | TTC | 1920 |
| Thr | Ile | Phe | Lys | Val | Arg | Met | Tyr | Val | Gly | Gly | Val | Glu | His | Arg | Phe | |
| 625 | | | | | 630 | | | | | 635 | | | | | 640 | |
| GAA | GCC | GCA | TGC | AAT | TGG | ACT | CGA | GGA | GAG | CGT | TGT | GAC | TTG | GAG | GAC | 1968 |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|--------|-----|-----|-----|-----|-----|-----|------|--|
| Glu | Ala | Ala | Cys | Asn | Trp | Thr | Arg | Gly | Glu | Arg | Cys | Asp | Leu | Glu | Asp | | |
| | | | | 645 | | | | | 650 | | | | | 655 | | | |
| AGG | GAT | AGA | TCA | GAG | CTT | AGC | CCG | CTG | CTG | CTG | TCT | ACA | ACA | GAG | TGG | 2016 | |
| Arg | Asp | Arg | Ser | Glu | Leu | Ser | Pro | Leu | Leu | Leu | Ser | Thr | Thr | Glu | Trp | | |
| | | | 660 | | | | | 665 | | | | | 670 | | | | |
| CAG | ATA | CTG | CCC | TGT | TCC | TTC | ACC | ACC | CTG | CCG | GCC | CTA | TCC | ACC | GGC | 2064 | |
| Gln | Ile | Leu | Pro | Cys | Ser | Phe | Thr | Thr | Leu | Pro | Ala | Leu | Ser | Thr | Gly | | |
| | | | 675 | | | | 680 | | | | | 685 | | | | | |
| CTG | ATC | CAC | CTC | CAT | CAG | AAC | ATC | GTG | GAC | GTG | CAA | TAC | CTG | TAC | GGT | 2112 | |
| Leu | Ile | His | Leu | His | Gln | Asn | Ile | Val | Asp | Val | Gln | Tyr | Leu | Tyr | Gly | | |
| | | | 690 | | | | 695 | | | | | 700 | | | | | |
| GTA | GGG | TCG | GCG | GTT | GTC | TCC | CTT | GTC | ATC | AAA | TGG | GAG | TAT | GTC | CTG | 2160 | |
| Val | Gly | Ser | Ala | Val | Val | Ser | Leu | Val | Ile | Lys | Trp | Glu | Tyr | Val | Leu | | |
| | 705 | | | | 710 | | | | | 715 | | | | | 720 | | |
| TTG | CTC | TTC | CTT | CTC | CTG | GCA | GAC | GCG | CGC | ATC | TGC | GCC | TGC | TTA | TGG | 2208 | |
| Leu | Leu | Phe | Leu | Leu | Leu | Ala | Asp | Ala | Arg | Ile | Cys | Ala | Cys | Leu | Trp | | |
| | | | | 725 | | | | | 730 | | | | | 735 | | | |
| ATG | ATG | CTG | CTG | ATA | GCT | CAA | GCT | GAG | GCC | GCC | TTA | GAG | AAC | CTG | GTG | 2256 | |
| Met | Met | Leu | Leu | Ile | Ala | Gln | Ala | Glu | Ala | Ala | Leu | Glu | Asn | Leu | Val | | |
| | | | 740 | | | | | 745 | | | | | 750 | | | | |
| GTC | CTC | AAT | GCG | GCG | GCC | GTG | GCC | GGG | GCG | CAT | GGC | ACT | CTT | TCC | TTC | 2304 | |
| Val | Leu | Asn | Ala | Ala | Ala | Val | Ala | Gly | Ala | His | Gly | Thr | Leu | Ser | Phe | | |
| | | | 755 | | | | 760 | | | | | 765 | | | | | |
| CTT | GTG | TTC | TTC | TGT | GCT | GCC | TGG | TAC | ATC | AAG | GGC | AGG | CTG | GTC | CCT | 2352 | |
| Leu | Val | Phe | Phe | Cys | Ala | Ala | Trp | Tyr | Ile | Lys | Gly | Arg | Leu | Val | Pro | | |
| | | | 770 | | | | 775 | | | | | 780 | | | | | |
| GGT | GCG | GCA | TAC | GCC | TTC | TAT | GGC | GTG | TGG | CCG | CTG | CTC | CTG | CTT | CTG | 2400 | |
| Gly | Ala | Ala | Tyr | Ala | Phe | Tyr | Gly | Val | Trp | Pro | Leu | Leu | Leu | Leu | Leu | | |
| | 785 | | | | 790 | | | | 795 | | | | | | 800 | | |
| CTG | GCC | TTA | CCA | CCA | CGA | GCT | TAT | GCC | TAGTAA | | | | | | | 2433 | |
| Leu | Ala | Leu | Pro | Pro | Arg | Ala | Tyr | Ala | | | | | | | | | |
| | | | | 805 | | | | | 810 | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Ser | Thr | Asn | Pro | Lys | Pro | Gln | Arg | Lys | Thr | Lys | Arg | Asn | Thr | Asn | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | |
| Arg | Arg | Pro | Gln | Asp | Val | Lys | Phe | Pro | Gly | Gly | Gly | Gln | Ile | Val | Gly | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | |
| Gly | Val | Tyr | Leu | Leu | Pro | Arg | Arg | Gly | Pro | Arg | Leu | Gly | Val | Arg | Ala | | |

| 35 | | | | | 40 | | | | | 45 | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Arg | Lys | Thr | Ser | Glu | Arg | Ser | Gln | Pro | Arg | Gly | Arg | Arg | Gln | Pro |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ile | Pro | Lys | Ala | Arg | Arg | Pro | Glu | Gly | Arg | Ala | Trp | Ala | Gln | Pro | Gly |
| | 65 | | | | | 70 | | | | | 75 | | | | 80 |
| Tyr | Pro | Trp | Pro | Leu | Tyr | Gly | Asn | Glu | Gly | Met | Gly | Trp | Ala | Gly | Trp |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Leu | Leu | Ser | Pro | Arg | Gly | Ser | Arg | Pro | Ser | Trp | Gly | Pro | Thr | Asp | Pro |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Arg | Arg | Arg | Ser | Arg | Asn | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Gly | Phe | Ala | Asp | Leu | Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Gly | Gly | Ala | Ala | Arg | Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp |
| | 145 | | | | | 150 | | | | | 155 | | | | 160 |
| Gly | Val | Asn | Tyr | Ala | Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Phe | Leu | Leu | Ala | Leu | Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | Ala | Tyr |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Glu | Val | Arg | Asn | Val | Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Asn | Ser | Ser | Ile | Val | Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr | Pro |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Gly | Cys | Val | Pro | Cys | Val | Arg | Glu | Asn | Asn | Ser | Ser | Arg | Cys | Trp | Val |
| | 225 | | | | | 230 | | | | | 235 | | | | 240 |
| Ala | Leu | Thr | Pro | Thr | Leu | Ala | Ala | Arg | Asn | Ala | Ser | Val | Pro | Thr | Thr |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Thr | Ile | Arg | Arg | His | Val | Asp | Leu | Leu | Val | Gly | Ala | Ala | Ala | Phe | Cys |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Ser | Ala | Met | Tyr | Val | Gly | Asp | Leu | Cys | Gly | Ser | Val | Phe | Leu | Val | Ser |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Gln | Leu | Phe | Thr | Ile | Ser | Pro | Arg | Arg | His | Glu | Thr | Val | Gln | Asp | Cys |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Asn | Cys | Ser | Ile | Tyr | Pro | Gly | His | Ile | Thr | Gly | His | Arg | Met | Ala | Trp |
| | 305 | | | | | 310 | | | | | 315 | | | | 320 |
| Asp | Met | Met | Met | Asn | Trp | Ser | Pro | Thr | Thr | Ala | Leu | Val | Val | Ser | Gln |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Leu | Leu | Arg | Ile | Pro | Gln | Ala | Val | Val | Asp | Met | Val | Ala | Gly | Ala | His |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Trp | Gly | Val | Leu | Ala | Gly | Leu | Ala | Tyr | Tyr | Ser | Met | Val | Gly | Asn | Trp |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Ala | Lys | Val | Leu | Val | Val | Met | Leu | Leu | Phe | Ala | Gly | Val | Asp | Gly | His |

| 370 | | | | | 375 | | | | | 380 | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Arg | Val | Ser | Gly | Gly | Ala | Ala | Ala | Ser | Asp | Thr | Arg | Gly | Leu | Val |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Ser | Leu | Phe | Ser | Pro | Gly | Ser | Ala | Gln | Lys | Ile | Gln | Leu | Val | Asn | Thr |
| | | | | 405 | | | | | 410 | | | | | 415 | |
| Asn | Gly | Ser | Trp | His | Ile | Asn | Arg | Thr | Ala | Leu | Asn | Cys | Asn | Asp | Ser |
| | | | 420 | | | | | 425 | | | | | 430 | | |
| Leu | Gln | Thr | Gly | Phe | Phe | Ala | Ala | Leu | Phe | Tyr | Lys | His | Lys | Phe | Asn |
| | | 435 | | | | | 440 | | | | | 445 | | | |
| Ser | Ser | Gly | Cys | Pro | Glu | Arg | Leu | Ala | Ser | Cys | Arg | Ser | Ile | Asp | Lys |
| | 450 | | | | | 455 | | | | | 460 | | | | |
| Phe | Ala | Gln | Gly | Trp | Gly | Pro | Leu | Thr | Tyr | Thr | Glu | Pro | Asn | Ser | Ser |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 |
| Asp | Gln | Arg | Pro | Tyr | Cys | Trp | His | Tyr | Ala | Pro | Arg | Pro | Cys | Gly | Ile |
| | | | | 485 | | | | | 490 | | | | | 495 | |
| Val | Pro | Ala | Ser | Gln | Val | Cys | Gly | Pro | Val | Tyr | Cys | Phe | Thr | Pro | Ser |
| | | | 500 | | | | | 505 | | | | | 510 | | |
| Pro | Val | Val | Val | Gly | Thr | Thr | Asp | Arg | Phe | Gly | Val | Pro | Thr | Tyr | Asn |
| | | 515 | | | | | 520 | | | | | 525 | | | |
| Trp | Gly | Ala | Asn | Asp | Ser | Asp | Val | Leu | Ile | Leu | Asn | Asn | Thr | Arg | Pro |
| | 530 | | | | | 535 | | | | | 540 | | | | |
| Pro | Arg | Gly | Asn | Trp | Phe | Gly | Cys | Thr | Trp | Met | Asn | Gly | Thr | Gly | Phe |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 |
| Thr | Lys | Thr | Cys | Gly | Gly | Pro | Pro | Cys | Asn | Ile | Gly | Gly | Ala | Gly | Asn |
| | | | | 565 | | | | | 570 | | | | | 575 | |
| Asn | Thr | Leu | Thr | Cys | Pro | Thr | Asp | Cys | Phe | Arg | Lys | His | Pro | Glu | Ala |
| | | | 580 | | | | | 585 | | | | | 590 | | |
| Thr | Tyr | Ala | Arg | Cys | Gly | Ser | Gly | Pro | Trp | Leu | Thr | Pro | Arg | Cys | Met |
| | | 595 | | | | | 600 | | | | | 605 | | | |
| Val | His | Tyr | Pro | Tyr | Arg | Leu | Trp | His | Tyr | Pro | Cys | Thr | Val | Asn | Phe |
| | 610 | | | | | 615 | | | | | 620 | | | | |
| Thr | Ile | Phe | Lys | Val | Arg | Met | Tyr | Val | Gly | Gly | Val | Glu | His | Arg | Phe |
| 625 | | | | | 630 | | | | | 635 | | | | | 640 |
| Glu | Ala | Ala | Cys | Asn | Trp | Thr | Arg | Gly | Glu | Arg | Cys | Asp | Leu | Glu | Asp |
| | | | | 645 | | | | | 650 | | | | | 655 | |
| Arg | Asp | Arg | Ser | Glu | Leu | Ser | Pro | Leu | Leu | Leu | Ser | Thr | Thr | Glu | Trp |
| | | | 660 | | | | | 665 | | | | | 670 | | |
| Gln | Ile | Leu | Pro | Cys | Ser | Phe | Thr | Thr | Leu | Pro | Ala | Leu | Ser | Thr | Gly |
| | | 675 | | | | | 680 | | | | | 685 | | | |
| Leu | Ile | His | Leu | His | Gln | Asn | Ile | Val | Asp | Val | Gln | Tyr | Leu | Tyr | Gly |
| | 690 | | | | | 695 | | | | | 700 | | | | |

Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu
 705 710 715 720

Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp
 725 730 735

Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val
 740 745 750

Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe
 755 760 765

Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro
 770 775 780

Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu
 785 790 795 800

Leu Ala Leu Pro Pro Arg Ala Tyr Ala
 805

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1..17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Ser Asn Ser Ser Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys
 1 5 10 15

Val

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1..22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Gly Gly Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 1 5 10 15
 Ser Pro Thr Thr Ala Leu
 20

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 1..37

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys
 1 5 10 15
 Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr
 20 25 30
 Pro Gly Cys Gly Lys
 35

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 1..25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Gly Gly Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr
 1 5 10 15
 Gln Leu Arg Arg His Ile Asp Leu Leu
 20 25

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: Modified-site
(B) LOCATION: 1..25

Gly Gly Thr Pro Thr Leu Ala Ala Arg Asp Ala Ser Val Pro Thr Thr
1 5 10 15
Thr Ile Arg Arg His Val Asp Leu Leu
20 25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Gln Val Arg Asn
1 5 10 15
Ser Thr Gly Leu
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp Cys Pro
1 5 10 15
Asn Ser Ser Ile
20

(2) INFORMATION FOR SEQ ID NO: 58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala His Asp Ala Ile
1          5          10          15
Leu His Thr Pro
                20

```

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr
1          5          10          15
Pro Gly Cys Val
                20

```

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

```

His Asp Ala Ile Leu His Thr Pro Gly Val Pro Cys Val Arg Glu Gly
1          5          10          15
Asn Val Ser

```

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

- Cys Val Arg Glu Gly Asn Val Ser Arg Cys Trp Val Ala Met Thr Pro
1 5 10 15
Thr Val Ala Thr
20

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr
1 5 10 15
Gln Leu Arg Arg
20

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear.

- (ii) MOLECULE TYPE: peptide

- Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser
1 5 10 15
Ala Thr Leu Cys
20

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

| | | | | | | | | | | | | | | | |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Val | Gly | Ser | Ala | Thr | Leu | Cys | Ser | Ala | Leu | Tyr | Val | Gly | Asp | Leu |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Cys Gly Ser Val | | | | | | | | | | | | | | | |
| 20 | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

| | | | | | | | | | | | | | | | |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Leu | Phe | Thr | Phe | Ser | Pro | Arg | Arg | His | Trp | Thr | Thr | Gln | Gly | Cys |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Asn Cys Ser Ile | | | | | | | | | | | | | | | |
| 20 | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

| | | | | | | | | | | | | | | | |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Gln | Gly | Cys | Asn | Cys | Ser | Ile | Tyr | Pro | Gly | His | Ile | Thr | Gly | His |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Arg Met Ala Trp | | | | | | | | | | | | | | | |
| 20 | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro
 1 5 10 15
 Thr Ala Ala Leu
 20

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

Asn Trp Ser Pro Thr Ala Ala Leu Val Met Ala Gln Leu Leu Arg Ile
 1 5 10 15
 Pro Gln Ala Ile
 20

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

Leu Leu Arg Ile Pro Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His
 1 5 10 15
 Trp Gly Val Leu
 20

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

Ala Gly Ala His Trp Gly Val Leu Ala Gly Ile Ala Tyr Phe Ser Met
1 5 10 15
Val Gly Asn Met
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala Glu Thr Ile Val Ser
1 5 10 15
Gly Gly Gln Ala
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

Ser Gly Leu Val Ser Leu Phe Thr Pro Gly Ala Lys Gln Asn Ile Gln
1 5 10 15
Leu Ile Asn Thr
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

Gln Asn Ile Gln Leu Ile Asn Thr Asn Gly Gln Trp His Ile Asn Ser
 1 5 10 15
 Thr Ala Leu Asn
 20

(2) INFORMATION FOR SEQ ID NO: 74:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

Leu Asn Cys Asn Glu Ser Leu Asn Thr Gly Trp Trp Leu Ala Gly Leu
 1 5 10 15
 Ile Tyr Gln His Lys
 20

(2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Ala Gly Leu Ile Tyr Gln His Lys Phe Asn Ser Ser Gly Cys Pro Glu
 1 5 10 15
 Arg Leu Ala Ser
 20

(2) INFORMATION FOR SEQ ID NO: 76:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Pro Leu Thr Asp Phe Asp

1 5 10 15
 Gln Gly Trp Gly
 20

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

Thr Asp Phe Asp Gln Gly Trp Gly Pro Ile Ser Tyr Ala Asn Gly Ser
 1 5 10 15

Gly Pro Asp Gln
 20

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

Ala Asn Gly Ser Gly Pro Asp Gln Arg Pro Tyr Cys Trp His Tyr Pro
 1 5 10 15

Pro Lys Pro Cys
 20

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Trp His Tyr Pro Pro Lys Pro Cys Gly Ile Val Pro Ala Lys Ser Val
 1 5 10 15

Cys Gly Pro Val

20

(2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

Ala Lys Ser Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val
 1 5 10 15

Val Val Gly Thr
 20

(2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Ser Gly Ala Pro Thr
 1 5 10 15

Tyr Ser Trp Gly
 20

(2) INFORMATION FOR SEQ ID NO: 82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

Gly Ala Pro Thr Tyr Ser Trp Gly Glu Asn Asp Thr Asp Val Phe Val
 1 5 10 15

Leu Asn Asn Thr
 20

(2) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

| | | | | | | | | | | | | | | | |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Asn | Trp | Phe | Gly | Cys | Thr | Trp | Met | Asn | Ser | Thr | Gly | Phe | Thr | Lys |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val Cys Gly Ala | | | | | | | | | | | | | | | |
| 20 | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

| | | | | | | | | | | | | | | | |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Phe | Thr | Lys | Val | Cys | Gly | Ala | Pro | Pro | Val | Cys | Ile | Gly | Gly | Ala |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Gly Asn Asn Thr | | | | | | | | | | | | | | | |
| 20 | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

| | | | | | | | | | | | | | | | |
|-------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Gly | Gly | Ala | Gly | Asn | Asn | Thr | Leu | His | Cys | Pro | Thr | Asp | Cys | Arg |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Lys His Pro | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Thr Asp Cys Phe Arg Lys His Pro Asp Ala Thr Tyr Ser Arg Cys Gly
1 5 10 15

Ser Gly Pro Trp
20

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

Ser Arg Cys Gly Ser Gly Pro Trp Ile Thr Pro Arg Cys Leu Val Asp
1 5 10 15

Tyr Pro Tyr Arg
20

(2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Cys Leu Val Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Ile
1 5 10 15

Asn Tyr Thr Ile
20

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

Pro Cys Thr Ile Asn Tyr Thr Ile Phe Lys Ile Arg Met Tyr Val Gly
 1 5 10 15
 Gly Val Glu His
 20

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Met Tyr Val Gly Gly Val Glu His Arg Leu Glu Ala Ala Cys Asn Trp
 1 5 10 15
 Thr Pro Gly Glu
 20

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Ala Cys Asn Trp Thr Pro Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp
 1 5 10 15
 Arg Ser Glu Leu
 20

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Thr Thr Thr
 1 5 10 15
 Gln Trp Gln Val
 20

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Tyr Gln Val Arg Asn Ser Thr Gly Leu
 1 5

(2) INFORMATION FOR SEQ ID NO: 94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

ACGTCCGTAC GTTCGAATTA ATTAATCGA

29

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

CCTCCGGACG TGCACTAGCT CCCGTCTGTG GTAGTGGTGG TAGTGATTAT CAATTAATTG

60

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

GTTTAACCAC TGCATGATG

19

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

GTCCCATCGA GTGCGGCTAC

20

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

CGTGACATGG TACATTCCGG ACACTTGGCG CACTTCATAA GCGGA

45

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

TGCCTCATAC ACAATGGAGC TCTGGGACGA GTCGTTCTGTG AC

42

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

TACCCAGCAG CGGGAGCTCT GTTGCTCCCG AACGCAGGGC AC

42

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

TGTCGTGGTG GGGACGGAGG CCTGCCTAGC TGCGAGCGTG GG

42

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

CGTTATGTGG CCCGGGTAGA TTGAGCACTG GCAGTCCTGC ACCGTCTC

48

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

CAGGGCCGTT CTAGGCCTCC ACTGCATCAT CATATCCCAA GC

42

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

CCGGAATGTA CCATGTCACG AACGAC

26

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:
GCTCCATTGT GTATGAGGCA GCGG

24

(2) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:
GAGCTCCCGC TGCTGGGTAG CGC

23

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:
CCTCCGTCCC CACCACGACA ATACG

25

(2) INFORMATION FOR SEQ ID NO: 108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

CTACCCGGGC CACATAACGG GTCACCG

27

(2) INFORMATION FOR SEQ ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

GGAGGCCTAC AACGGCCCTG GTGG

24

(2) INFORMATION FOR SEQ ID NO: 110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

TTCTATCGAT TAAATAGAAT TC

22

(2) INFORMATION FOR SEQ ID NO: 111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid

(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO

23

(2) INFORMATION FOR SEQ ID NO: 112:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys
 1 5 10 15
 Ser Asn Ser Ser
 20

(2) INFORMATION FOR SEQ ID NO: 113:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp
 1 5 10 15
 Met Ile Met His Thr
 20

(2) INFORMATION FOR SEQ ID NO: 114:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val
 1 5 10 15

Arg Glu Asn Asn Ser
20

(2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu
 1 5 10 15

Thr Pro Thr Leu Ala
 20

(2) INFORMATION FOR SEQ ID NO: 116:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro
 1 5 10 15

Thr Thr Thr Ile Arg
 20

(2) INFORMATION FOR SEQ ID NO: 117:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

| | | | | | | | | | | | | | | |
|---------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Val | Pro | Thr | Thr | Thr | Ile | Arg | Arg | His | Val | Asp | Leu | Leu | Val |
| 1 | | | | | 5 | | | | 10 | | | | | 15 |
| Gly Ala Ala Ala Phe | | | | | | | | | | | | | | |
| 20 | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

| | | | | | | | | | | | | | | |
|---------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Val | Gly | Ala | Ala | Ala | Phe | Cys | Ser | Ala | Met | Tyr | Val | Gly |
| 1 | | | | | 5 | | | | 10 | | | | | 15 |
| Asp Leu Cys Gly Ser | | | | | | | | | | | | | | |
| 20 | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

| | | | | | | | | | | | | | | |
|---------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Val | Gly | Asp | Leu | Cys | Gly | Ser | Val | Phe | Leu | Val | Ser | Gln | Leu |
| 1 | | | | | 5 | | | | 10 | | | | | 15 |
| Phe Thr Ile Ser Pro | | | | | | | | | | | | | | |
| 20 | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gln | Leu | Phe | Thr | Ile | Ser | Pro | Arg | Arg | His | Glu | Thr | Val | Gln |
| 1 | | | | | 5 | | | | 10 | | | | | 15 |

| | | | | |
|-----|-----|-----|-----|-----|
| Asp | Cys | Asn | Cys | Ser |
| | | | | 20 |

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Val | Gln | Asp | Cys | Asn | Cys | Ser | Ile | Tyr | Pro | Gly | His | Ile | Thr |
| 1 | | | | | 5 | | | | 10 | | | | | 15 |

| | | | | |
|-----|-----|-----|-----|-----|
| Gly | His | Arg | Met | Ala |
| | | | | 20 |

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Ile | Thr | Gly | His | Arg | Met | Ala | Trp | Asp | Met | Met | Met | Asn | Trp |
| 1 | | | | | 5 | | | | 10 | | | | | 15 |

| | | | | |
|-----|-----|-----|-----|-----|
| Ser | Pro | Thr | Thr | Ala |
| | | | | 20 |

Cancelled